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(54) Title: LFA-1 REGULATORY BINDING SITE AND USES THEREOF			
(57) Abstract Methods to negatively regulate LFA-1 binding to an ICAM that binds LFA-1 are provided, in addition to a novel regulatory binding site on LFA-1.			

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LFA-1 REGULATORY BINDING SITE AND USES THEREOF

BACKGROUND

The leukocyte function-associated antigen (LFA-1, CD11a/CD18) is a leukocyte-specific β_2 integrin that participates in cell/cell adhesion. Binding activity of LFA-1 is essential to leukocyte extravasation from circulation to a site of injury in an inflammatory response. Three principle ligands are known to bind LFA-1, ICAM-1, ICAM-2, and ICAM-3. These are intercellular adhesion molecules that play an important role in localizing leukocyte adhesion to endothelial cells at a site of injury. ICAM-4 and ICAM-5 have also been reported to bind LFA-1. Most leukocytes constitutively express LFA-1, but ligand binding requires activation believed to induce a conformational change and to increase avidity ligand binding. For example, ICAM-1 is normally expressed at low levels on the endothelium. However, injury-induced inflammatory mediators promote enhanced surface expression in cells at the site of the injury which, in turn, promotes localized leukocyte adhesion through binding to activated LFA-1.

The structure of LFA-1 includes distinct intracellular and extracellular domains that are believed to participate in and/or regulate ICAM binding. Of particular interest is a region in the α_L chain of approximately 200 amino acids, designated the I domain, that is found in all β_2 integrins, as well as many other proteins. Evidence suggests that the I domain is essential to LFA-1 binding to ICAM-1 and 3. For example, anti-LFA-1 blocking monoclonal antibodies have been mapped to epitopes within the I domain. In addition, recombinant I domain polypeptide fragments have been shown to inhibit integrin-mediated adhesion and bind ICAM-1. Within the I domain of LFA-1 (and other proteins) is a single metal ion dependent adhesion site (MIDAS) that preferentially binds manganese or magnesium ions.

Binding of either cation is required for ligand interaction and is believed to induce conformational changes in LFA-1 necessary for binding. Cation binding may therefore be a regulatory mechanism that responds to changes in the extracellular leukocyte environment. This hypothesis is supported by the observation that calcium ion binding actually inhibits LFA-1 interaction with ICAM-1. Indeed, it has been

proposed that an inactive LFA-1 conformation results from calcium binding, and that replacement of the calcium ion with a manganese or magnesium ion is a step required for LFA-1 activation [Griggs, *et al.*, *J. Biol. Chem.* 273:22113-22119 (1998)]. Other factors have also been shown to induce LFA-1 activation, including T cell receptor engagement, cytokine stimulation, and *in vitro* PMA stimulation.

In practical terms, the identification of LFA-1/ICAM binding sites provides targets to modulate leukocyte inflammatory responses. Numerous antibodies have been isolated that are capable of inducing LFA-1 activation [see, for example, Landis, *et al.*, *J. Cell Biol.* 120:1519-1527 (1993)] or that are capable of preventing ICAM-1 interaction [see for example, Randi and Hogg, *J. Biol. Chem.* 269:12395-12398 (1994)]. The previous identification of anti-LFA-1 activating antibodies that recognize multiple and distinct extracellular epitopes suggests the existence of more than one regulatory region, presumably independent of cytoplasmic signaling.

Localization of LFA-1 sites that bind ICAM-1 has been investigated through use of chimeric LFA-1 α subunit proteins comprising human and murine components [Huang and Springer, *J. Biol. Chem.* 270:19008-19016 (1995)]. Studies have indicated that residues that coordinate cation binding and residues proximal to the site are essential for binding ICAM-1 at a relatively flat interface. More precise delineation of the extracellular regulatory region(s) and the contact points for ICAM-1 binding will permit design of efficient modulators.

Thus there exists a need in the art to precisely identify regulatory regions for proteins that participate in inflammatory responses, and in particular LFA-1 and ICAMs that bind LFA-1. Determining the tertiary (or quaternary) structure of a protein can identify potential regulatory regions to permit the rational design of biologically compatible small molecules for therapeutic and prophylactic intervention for inflammatory disorders. There further exists a need in the art to identify compounds that can inhibit LFA-1 binding to ICAMs that can be used in the treatment of inflammatory disorders.

SUMMARY OF THE INVENTION

The present invention provides methods for identifying a negative regulator of LFA-1 binding to a natural ligand that competes for binding to LFA-1 with ICAM-1 or ICAM-3 comprising the steps of (i) contacting LFA-1, or a ligand binding fragment thereof, and a ligand that binds LFA-1, or an LFA-1-binding fragment thereof, in the presence and absence of a test compound under conditions that allow binding of LFA-1 to the ligand (ii) identifying as a negative regulator the compound which decreases LFA-1 binding to the ligand and which binds LFA-1 α_L polypeptide at a site presenting a diaryl sulfide binding conformation defined by Ile²⁵⁹, Leu²⁹⁸, Ile²³⁵, Val¹⁵⁷, Leu¹⁶¹, and Ile³⁰⁶ of human LFA-1 as set out in SEQ ID NO: 2, which provides the amino acid sequence for mature (*i.e.*, without the leader sequence) LFA-1. “Natural ligand” refers to any biological compound that binds LFA-1. The term “negative regulator” refers to a compound that decreases ICAM binding to LFA-1, but does not directly compete with the ICAM for LFA-1 binding. A negative regulator may be an allosteric inhibitor or a compound that modulates the activation state of LFA-1. In a preferred method, the negative regulator is a diaryl sulfide. In a preferred embodiment, the natural ligand is an ICAM. Most preferably, the ICAM is ICAM-1 or ICAM-3.

In another aspect, the invention provides methods for identifying a negative regulator of LFA-1 binding to a natural ligand that binds LFA-1 comprising the steps of (i) contacting LFA-1, or a ligand binding fragment thereof, and a natural ligand that binds LFA-1, or an LFA-1-binding fragment thereof, in the presence and absence of a test compound under conditions that allow binding of LFA-1 to the ligand, (ii) identifying as a negative regulator the compound which decreases LFA-1 binding to the ligand and which competes with (2-isopropyl-phenyl)[2-nitro-4-(E-((4-acetyl-piperazin-1-yl)carbonyl)ethenyl)phenyl]sulfide for binding to LFA-1 α_L polypeptide. In a preferred method, the negative regulator is a diaryl sulfide. Preferably, the ligand is an ICAM. Most preferably, the ICAM is ICAM-1 or ICAM-3.

The invention also provides screening methods for identifying a negative regulator of LFA-1 binding to a natural ligand that binds LFA-1 comprising

the steps of (i) contacting LFA-1, or a ligand binding fragment thereof, with (2-isopropyl-phenyl)[2-nitro-4-(E-((4-acetyl-piperazin-1-yl)carbonyl)ethenyl)phenyl]-sulfide in the presence and absence of a compound, and (ii) identifying the compound as a putative negative regulator wherein the compound competes with (2-isopropyl-phenyl)[2-nitro-4-(E-((4-acetyl-piperazin-1-yl)carbonyl)ethenyl)phenyl]-sulfide for binding to LFA-1 α_L polypeptide. In a preferred method, the negative regulator is a diaryl sulfide.

The invention also provides pharmaceutical compositions comprising a negative regulator of LFA-1 binding to a natural ligand that binds LFA-1 identified by a method of the invention. The invention further provides use of a negative regulator identified by a method of the invention in the production of a medicament to ameliorate pathologies arising from LFA-1 binding to an ICAM that binds LFA-1.

The invention further provides methods for inhibiting LFA-1 binding to a natural ligand that binds LFA-1 comprising the step of contacting LFA-1, or a ligand binding fragment thereof, with a negative regulator compound; said negative regulator binding the LFA-1 α_L polypeptide, or a fragment thereof, at a site selected from the group consisting of a conformation that binds a diaryl sulfide, a site defined by Ile²⁵⁹, Leu²⁹⁸, Ile²³⁵, Val¹⁵⁷, Leu¹⁶¹, and Ile³⁰⁶ of human LFA-1 α_L polypeptide, and an LFA-1 domain that binds (2-isopropyl-phenyl)[2-nitro-4-(E-((4-acetyl-piperazin-1-yl)carbonyl)ethenyl)phenyl]sulfide . In a preferred method, the negative regulator is a diaryl sulfide. In one embodiment, methods of the invention include use of cells expressing either LFA-1 or the ligand. In methods wherein one of the binding partners is expressed in a cell, the other binding partner is either purified and isolated, in a fluid sample (purified, partially purified, or crude) taken from an individual, or in a cell lysate. The invention also comprehends methods wherein both LFA-1 and the ICAM are expressed in cells. The LFA-1 and ligand binding partners may be expressed on the same cell type or different cell types.

The invention also provides methods to inhibit leukocyte adhesion to endothelial cells comprising the step of contacting said leukocyte with a negative regulator of LFA-1 binding to a natural ligand that binds LFA-1, said negative regulator binding an LFA-1 regulatory site selected from the group consisting of a site

that binds a diaryl sulfide, a site defined by Ile²⁵⁹, Leu²⁹⁸, Ile²³⁵, Val¹⁵⁷, Leu¹⁶¹, and Ile³⁰⁶ of human LFA-1 α_L polypeptide, and an LFA-1 domain that binds (2-isopropyl-phenyl)[2-nitro-4-(E-((4-acetylpirazin-1-yl)carbonyl)ethenyl)phenyl]sulfide. *In vivo* and *in vitro* methods are contemplated. In a presently preferred embodiment, the negative regulator of the methods is a diaryl sulfide and the regulatory binding is reversible.

The invention also provides methods to ameliorate a pathology arising from LFA-1 binding to a natural ligand that binds LFA-1 comprising the step of administering to an individual in need thereof a negative regulator of LFA-1 binding to the ligand in an amount effective to inhibit LFA-1 binding to the ligand, said negative regulator binding to an LFA-1 regulatory site selected from the group consisting of a site that binds a diaryl sulfide, a site defined by Ile²⁵⁹, Leu²⁹⁸, Ile²³⁵, Val¹⁵⁷, Leu¹⁶¹, and Ile³⁰⁶ of human LFA-1 and an LFA-1 domain that binds compound (2-isopropyl-phenyl)[2-nitro-4-(E-((4-acetylpirazin-1-yl)carbonyl)ethenyl)phenyl]-sulfide.

The invention also provides LFA-1 α_L polypeptides and fragments thereof comprising a regulatory binding site presenting a diaryl sulfide binding conformation. In one aspect, the LFA-1 polypeptide fragment comprises the α_L polypeptide I domain sequence. Preferably, the LFA-1 polypeptide contains less than all amino acids in the α polypeptide I domain. The invention also provides mutant LFA-1 polypeptides wherein amino acid residues in the wild type α_L polypeptide regulatory site are substituted with non-naturally occurring (*i.e.*, residues not found in the same position in the wild type molecule) amino acid residues. Preferred mutant regulatory sites exhibit modified affinity and/or avidity for an ICAM, both in the presence and absence of an inducing agent (*e.g.*, the monoclonal antibody 240Q described below which induces LFA-1 into an activated state required for ICAM binding). Presently preferred mutants include (i) those demonstrating wild type levels of ICAM-1 binding with or without monoclonal antibody 240Q induction, exemplified mutations having one or more of the single amino acid changes Val¹⁵⁷-Ala, Glu²¹⁸-Ala, Thr²³¹-Ala, Lys²⁸⁰-Ala, and Lys²⁹⁴-Ala, (ii) mutants that support greater than wild type levels of binding without induction and wild type levels

with induction, exemplified by mutations having one or more of the single amino acid changes Ile²³⁵-Ala, Ile²⁵⁵-Ala, Ser²⁸³-Ala, Glu²⁸⁴-Ala, Glu³⁰¹-Ala, and Ile³⁰⁶-Ala,
5 (iii) mutants with decreased levels of ICAM-1 binding relative to wild type binding in the absence of induction, but wild-type levels with antibody 240Q induction,
exemplified by mutants having one or more of the substitutions Lys¹⁶⁰-Ala,
Lys²³²-Ala, Asp²⁵³-Ala, Lys²⁸⁷-Ala, Gln³⁰³-Ala, Lys³⁰⁴-Ala, and Lys³⁰⁵-Ala, and
(iv) mutants demonstrating severely decreased levels or no ICAM-1 binding with or without induction, exemplified by a mutant with the single substitution Tyr³⁰⁷-Ala:

10 The invention also provides an LFA-1-activating monoclonal antibody secreted by a hybridoma designated 240Q, mailed on March 30, 1999 to, and received on March 31, 1999 by the American Type Culture Collection, 10861 University Blvd., Manassas, VA 20010-2209, and assigned Accession No: HB-12692.

DETAILED DESCRIPTION OF THE INVENTION

15 The present invention provides novel *in vivo* and *in vitro* methods for negatively, and preferably reversibly, regulating LFA-1 binding to a natural ligand that binds LFA-1 involving use of compounds which bind LFA-1 at a regulatory domain located remote from the ligand binding site. The LFA-1 regulatory site presents a conformation that binds a substituted diaryl sulfide. The binding site is defined by 20 human LFA-1 amino acid residues Ile²⁵⁹, Leu²⁹⁸, Ile²³⁵, Val¹⁵⁷, Leu¹⁶¹ and Ile³⁰⁶. Alternatively, the site is defined by amino acid residues Ile²⁵⁹, Leu²⁹⁸, Ile²³⁵, Val¹⁵⁷, 25 Leu¹⁶¹ Ile³⁰⁶, Leu³⁰², Tyr²⁵⁷, Leu¹³², Val²³³, Val¹³⁰, and Tyr¹⁶⁶. In still another alternative, the binding site is defined by amino acid residues Lys²⁸⁷, Leu²⁹⁸, Ile²⁵⁹, Leu³⁰², Ile²³⁵, Val¹⁵⁷, Tyr²⁵⁷, Lys³⁰⁵, Leu¹⁶¹, Leu¹³², Val²³³, Ile²⁵⁵, Val¹³⁰, Tyr¹⁶⁶, Ile³⁰⁶, Phe¹³⁴, Phe¹⁶⁸, Phe¹⁵³, Tyr³⁰⁷, Val³⁰⁸, Ile³⁰⁹, Thr²³¹, Glu²⁸⁴, Phe²⁸⁵, Glu³⁰¹, Met¹⁵⁴, Ile²³⁷, Ile¹⁵⁰, and Leu²⁹⁵. Preferably, the ligand is an ICAM. Most preferably, the ICAM is ICAM-1 or ICAM-3.

30 In a presently preferred embodiment, reversible negative regulation (*i.e.*, reversible inhibition) of LFA-1 binding to ligand ICAM is provided by substituted diaryl sulfide compounds which bind LFA-1 at the aforementioned

regulatory domain and/or compounds that competitively inhibit diaryl sulfide binding to said domain.

In one aspect, methods of the invention are carried out using LFA-1 and a binding partner protein, such as ICAM-1, which are recombinant, purified from natural sources, or synthetic. In a preferred method of the invention, the LFA-1 and ICAM binding partner proteins are recombinant. The binding partner proteins may be holoproteins (*e.g.*, including both α and β chains of LFA-1), protein subunits (*e.g.*, the isolated LFA-1 α polypeptide chain), or fragments thereof, including, for example, extracellular domains of either LFA-1 or the ICAM, I domain fragments of LFA-1, less than complete I domain fragments of LFA-1, and/or less than a complete extracellular domain of the ICAM.

In another aspect, the invention provides methods wherein either LFA-1, the ligand, or both are expressed in a cell. When one or both binding partner proteins are expressed in a cell, the cell can be one that expresses an endogenous polynucleotide encoding LFA-1 or the ligand, or a host cell transformed and transfected with a heterologous polynucleotide encoding LFA-1 or the ligand and grown under conditions appropriate to permit expression of LFA-1 or the ligand on the cell surface. Regardless of whether cells of the methods express endogenous or heterologous polynucleotides encoding LFA-1 or the ligand, transcription of the polynucleotide can be directed by either endogenous or heterologous transcriptional control elements. For example, endogenous control elements can be purified from a desired host cell and ligated in an operative position relative to the LFA-1 or the ligand-encoding polynucleotide. Alternatively, a cell expressing endogenous LFA-1 or the ligand can be modified, for example through homologous recombination, to provide the LFA-1 or ligand polynucleotide with one or more transcriptional control elements that modify wild type levels of proteins expression. In assays involving cells expressing endogenous LFA-1 and ligand, preferred cells are leukocytes, *i.e.*, lymphocytes, monocytes, and granulocytes (*e.g.*, neutrophils), and endothelial cells.

In another aspect, the invention embraces methods to inhibit leukocyte adhesion to endothelial cells associated with LFA-1, expressed on leukocytes, binding to an ICAM that binds LFA-1, expressed on endothelial cells. Leukocyte adhesion to

endothelium is characteristic of an inflammatory response arising from release of cell mediators at an injury site. By providing methods to inhibit leukocyte adhesion to endothelial cells, the invention also comprehends methods to inhibit an inflammatory response associated with LFA-1 binding to a natural ligand that binds LFA-1.

5

Therapeutic Methods

To the extent that leukocyte adhesion to endothelial cells gives rise to a pathological disorder, the invention provides methods to ameliorate pathologies associated with accumulation of leukocytes resulting from LFA-1 binding to an ICAM that binds LFA-1, comprising the step of administering to an individual in need thereof an amount of an inhibitor of LFA-1 binding to the ICAM effective to inhibit LFA-1 binding to the ICAM, said inhibitor binding to LFA-1 at a site presented by amino acid residues Ile²⁵⁹, Leu²⁹⁸, Ile²³⁵, Val¹⁵⁷, Leu¹⁶¹ and Ile³⁰⁶. Exemplary medical conditions include, without limitation, inflammatory diseases, autoimmune diseases, reperfusion injury, myocardial infarction, stroke, hemorrhagic shock, organ transplant, and the like. Methods of the invention provide for amelioration of a variety of pathologies, including, for example, but not limited to adult respiratory distress syndrome, multiple organ injury syndrome secondary to septicemia, multiple organ injury secondary to trauma, reperfusion injury of tissue, acute glomerulonephritis, reactive arthritis, dermatosis with acute inflammatory components, stroke, thermal injury, Crohn's disease, necrotizing enterocolitis, granulocyte transfusion associated syndrome, cytokine induced toxicity, and T cell mediated diseases.

Inflammatory cell activation and excessive or unregulated cytokine (e.g., TNF α and IL-1 β) production are also implicated in disorders such as rheumatoid arthritis, osteoarthritis, gouty arthritis, spondylitis, thyroid associated ophthalmopathy, Behcet disease, sepsis, septic shock, endotoxic shock, gram negative sepsis, gram positive sepsis, toxic shock syndrome, asthma, chronic bronchitis, allergic respiratory distress syndrome, chronic pulmonary inflammatory disease, such as chronic obstructive pulmonary disease, silicosis, pulmonary sarcoidosis, reperfusion injury of the myocardium, brain, and extremities, fibrosis, cystic fibrosis, keloid formation, scar formation, atherosclerosis, transplant rejection disorders, such as graft vs. host

reaction and allograft rejection, chronic glomerulonephritis, lupus, inflammatory bowel disease, such as ulcerative colitis, proliferative lymphocyte diseases, such as leukemia, and inflammatory dermatoses, such as atopic dermatitis, psoriasis, urticaria, and uveitis.

5 Other conditions characterized by elevated cytokine levels include brain injury due to moderate trauma (see *J. Neurotrauma*, 12, pp. 1035-1043 (1995); *J. Clin. Invest.*, 91, pp. 1421-1428 (1993)), cardiomyopathies, such as congestive heart failure (see *Circulation*, 97, pp. 1340-1341 (1998)), cachexia, cachexia secondary to infection or malignancy, cachexia secondary to acquired immune 10 deficiency syndrome (AIDS), ARC (AIDS related complex), fever myalgias due to infection, cerebral malaria, osteoporosis and bone resorption diseases, keloid formation, scar tissue formation, and pyrexia.

The ability of the negative regulators of the invention to treat arthritis can be demonstrated in a murine collagen-induced arthritis model [Kakimoto, *et al.* 15 *Immunol.* 142:326-337 (1992)], in a rat collagen-induced arthritis model [Knoerzer, *et al.*, *Toxical Pathol.* 25:13-19 (1997)], in a rat adjuvant arthritis model [Halloran, *et al.*, *Arthritis Rheum* 39:810-819 (1996)], in a rat streptococcal cell wall-induced 20 arthritis model [Schimmer, *et al.*, *J. Immunol.* 160:1466-1477 (1998)], or in a SCID-mouse human rheumatoid arthritis model [Oppenheimer-Marks, *et al.*, *J. Clin. Invest.* 101:1261-1272 (1998)].

The ability of the negative regulators to treat Lyme arthritis can be demonstrated according to the method of Gross, *et al.*, *Science*, 218:703-706, (1998).

The ability of the negative regulators to treat asthma can be demonstrated in a murine allergic asthma model according to the method of Wegner, *et al.*, *Science*, 247:456-459, (1990), or in a murine non-allergic asthma model 25 according to the method of Bloemen, *et al.*, *Am. J. Respir. Crit. Care Med.* 153:521-529 (1996).

The ability of the negative regulators to treat inflammatory lung injury can be demonstrated in a murine oxygen-induced lung injury model according to the 30 method of Wegner, *et al.*, *Lung*, 170:267-279, (1992), in a murine immune complex-induced lung injury model according to the method of Mulligan, *et al.*, *J. Immunol.*,

154:1350-1363, (1995), or in a murine acid-induced lung injury model according to the method of Nagase, *et al.*, *Am. J. Respir. Crit. Care Med.*, 154:504-510, (1996).

5 The ability of the negative regulators to treat inflammatory bowel disease can be demonstrated in a murine chemical-induced colitis model according to the method of Bennett, *et al.*, *J. Pharmacol. Exp. Ther.*, 280:988-1000, (1997).

The ability of the negative regulators to treat autoimmune diabetes can be demonstrated in an NOD mouse model according to the method of Hasagawa, *et al.*, *Int. Immunol.* 6:831-838 (1994), or in a murine streptozotocin-induced diabetes model according to the method of Herold, *et al.*, *Cell Immunol.* 157:489-500, (1994).

10 The ability of the negative regulators to treat inflammatory liver injury can be demonstrated in a murine liver injury model according to the method of Tanaka, *et al.*, *J. Immunol.*, 151:5088-5095, (1993).

15 The ability of the negative regulators to treat inflammatory glomerular injury can be demonstrated in a rat nephrotoxic serum nephritis model according to the method of Kawasaki, *et al.*, *J. Immunol.*, 150:1074-1083 (1993).

The ability of the negative regulators to treat radiation-induced enteritis can be demonstrated in a rat abdominal irradiation model according to the method of Panes, *et al.*, *Gastroenterology*, 108:1761-1769 (1995).

20 The ability of the negative regulators to treat radiation pneumonitis can be demonstrated in a murine pulmonary irradiation model according to the method of Hallahan, *et al.*, *Proc. Natl. Acad. Sci. (USA)*, 94:6432-6437 (1997).

25 The ability of the negative regulators to treat reperfusion injury can be demonstrated in the isolated heart according to the method of Tamiya, *et al.*, *Immunopharmacology*, 29:53-63 (1995), or in the anesthetized dog according to the model of Hartman, *et al.*, *Cardiovasc. Res.* 30:47-54 (1995).

30 The ability of the negative regulators to treat pulmonary reperfusion injury can be demonstrated in a rat lung allograft reperfusion injury model according to the method of DeMeester, *et al.*, *Transplantation*, 62:1477-1485 (1996), or in a rabbit pulmonary edema model according to the method of Horgan, *et al.*, *Am. J. Physiol.* 261:H1578-H1584 (1991).

The ability of the negative regulators to treat stroke can be demonstrated in a rabbit cerebral embolism stroke model according to the method of Bowes, *et al.*, *Exp. Neurol.*, 119:215-219 (1993), in a rat middle cerebral artery ischemia-reperfusion model according to the method of Chopp, *et al.*, *Stroke*, 25:869-875 (1994), or in a rabbit reversible spinal cord ischemia model according to the method of Clark *et al.*, *Neurosurg.*, 75:623-627 (1991). The ability of the negative regulators to treat cerebral vasospasm can be demonstrated in a rat experimental vasospasm model according to the method of Oshiro, *et al.*, *Stroke*, 28:2031-2038 (1997).

10 The ability of the negative regulators to treat peripheral artery occlusion can be demonstrated in a rat skeletal muscle ischemia/reperfusion model according to the method of Gute, *et al.*, *Mol. Cell Biochem.*, 179:169-187 (1998).

15 The ability of the negative regulators to treat graft rejection can be demonstrated in a murine cardiac allograft rejection model according to the method of Isobe, *et al.*, *Science*, 255:1125-1127 (1992), in a murine thyroid gland kidney capsule model according to the method of Talento, *et al.*, *Transplantation*, 55:418-422 (1993), in a cynomolgus monkey renal allograft model according to the method of Cosimi, *et al.*, *J. Immunol.*, 144:4604-4612 (1990), in a rat nerve allograft model according to the method of Nakao, *et al.*, *Muscle Nerve*, 18:93-102 (1995), in a murine skin allograft model according to the method of Gorczynski and Wojcik, *J. Immunol.* 152:2011-2019, (1994), in a murine corneal allograft model according to the method of He, *et al.*, *Ophthalmol. Vis. Sci.*, 35:3218-3225 (1994), or in a xenogeneic pancreatic islet cell transplantation model according to the method of Zeng, *et al.*, *Transplantation*, 58:681-689 (1994).

20 25 The ability of the negative regulators to treat graft-vs.-host disease (GVHD) can be demonstrated in a murine lethal GVHD model according to the method of Harming, *et al.*, *Transplantation*, 52:842-845 (1991).

30 The ability of the negative regulators to treat cancers can be demonstrated in a human lymphoma metastasis model (in mice) according to the method of Aoudjit, *et al.*, *J. Immunol.*, 161:2333-2338, (1998).

Regulatory Binding Site

The invention also provides an LFA-1 regulatory binding site. The regulatory binding site is displayed on the α_L chain of LFA-1 in its wild type, or native, conformation. Fragments of the α_L chain that display the regulatory site are also contemplated, and preferred fragments of the invention include α_L chain I domain sequences, as well as fragments consisting of less than a complete α_L chain I domain. 5 The invention provides LFA-1 regulatory binding sites as part of a polypeptide comprising a human LFA-1 amino acid sequence, the amino acid sequence of a species homolog of human LFA-1, the amino acid sequence of analogs of human LFA-1, or the amino acid sequence of a synthetic polypeptide with homology to 10 human LFA-1. Regulatory binding sites displayed on synthetic polypeptide-like mimetics are also contemplated.

The regulatory binding site of the invention binds a diaryl sulfide (alternatively referred to as a diaryl thioether compound) comprising a first aryl ring and second aryl ring linked to one another through a sulfur atom. In one aspect, the 15 site is defined by human LFA-1 amino acid residues Ile²⁵⁹, Leu²⁹⁸, Ile²³⁵, Val¹⁵⁷, Leu¹⁶¹ and Ile³⁰⁶. Alternatively, the binding site is defined by other amino acid residues (*i.e.*, conservative substitutions) or compounds that mimic the binding ability of a site defined by LFA-1 Ile²⁵⁹, Leu²⁹⁸, Ile²³⁵, Val¹⁵⁷, Leu¹⁶¹ and Ile³⁰⁶. The regulatory site is 20 also defined by LFA-1 α_L polypeptide amino acid residues that present a domain that binds (2-isopropyl-phenyl)[2-nitro-4-(E-((4-acetyl-piperazin-1-yl)carbonyl)ethenyl)-phenyl]sulfide. Preferably, the regulatory site of the invention reversibly binds a negative regulator compound.

The invention also provides LFA-1 regulatory binding site mutants 25 wherein one or more amino acid residues defining the site (*i.e.*, presenting the (2-isopropyl-phenyl)[2-nitro-4-(E-((4-acetyl-piperazin-1-yl)carbonyl)ethenyl)-phenyl]-sulfide binding site) is substituted with an alternative amino acid residue, wherein substitution of the wild type amino acid residues results in modified capacity for the mutant to bind (2-isopropyl-phenyl)[2-nitro-4-(E-((4-acetyl-piperazin-1-yl)carbonyl)-ethenyl)-phenyl]sulfide compared to a wild type regulatory site. Preferred mutant 30 regulatory sites exhibit modified affinity and/or avidity for ICAM-1, both in the

presence and absence of an agent that induces ICAM-1 binding (e.g., the monoclonal antibody 240Q which induces LFA-1 into an activated state required for ICAM binding). Presently preferred mutants include (i) those demonstrating wild type levels of ICAM-1 binding with or without monoclonal antibody 240Q induction,

5 exemplified by mutants having one or more of the amino acid changes Val¹⁵⁷-Ala, Glu²¹⁸-Ala, Thr²³¹-Ala, Lys²⁸⁰-Ala, and Lys²⁹⁴-Ala, (ii) mutants that support greater than wild type levels of binding without induction and wild type levels with induction, exemplified by mutants having one or more of the amino acid changes Ile²³⁵-Ala, Ile²⁵⁵-Ala, Ser²⁸³-Ala, Glu²⁸⁴-Ala, Glu³⁰¹-Ala, and Ile³⁰⁶-Ala, (iii) mutants with

10 decreased levels of ICAM-1 binding relative to wild type in the absence of induction, but wild-type levels with antibody 240Q induction, exemplified by mutants having one or more of the amino acid substitutions Lys¹⁶⁰-Ala, Lys²³²-Ala, Asp²⁵³-Ala, Lys²⁸⁷-Ala, Gln³⁰³-Ala, Lys³⁰⁴-Ala, and Lys³⁰⁵-Ala, and (iv) mutants demonstrating severely decreased levels or no ICAM-1 binding with or without induction,

15 exemplified by a mutant with the substitution Tyr³⁰⁷-Ala.

Mutants of the LFA-1 regulatory site are useful in production of antibodies that more precisely define LFA-1 epitopes that can serve as targets for therapeutic intervention. As another example, soluble regulatory sites (or LFA-1 regulatory sites as part of chimeric compounds) with an increased ability to bind an ICAM that binds LFA-1 can modulate LFA-1 binding to the ICAM through competitive inhibition.

Screening Methods

The invention further provides methods for identifying a negative regulator of LFA-1 binding to an ICAM that binds LFA-1 comprising the steps of (i) contacting LFA-1 and the ICAM in the presence and absence of a test compound under conditions that allow binding of LFA-1 to the ICAM, (ii) identifying as a negative regulator the compound which decreases LFA-1 binding to the ICAM and which binds LFA-1 α_L polypeptide at a site presenting a diaryl sulfide binding conformation defined by Ile²⁵⁹, Leu²⁹⁸, Ile²³⁵, Val¹⁵⁷, Leu¹⁶¹, and Ile³⁰⁶ of human LFA-1.

25 An IC₅₀ value for a compound is defined as the concentration of the compound

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required to produce 50% inhibition of a biological activity of interest. As used herein, a negative regulator is defined as a compound characterized by an IC₅₀ for inhibition of LFA-1 binding to a natural ligand. Negative regulators of LFA-1 binding are defined to have an IC₅₀ of less than about 200 μM, less than about 100 μM, less than about 50 μM, and preferably from about 0.05 μM to 40 μM. In another aspect, the invention provides methods for identifying a negative regulator of LFA-1 binding to an ICAM that binds LFA-1 comprising the steps of (i) contacting LFA-1 and the ICAM under conditions that allow binding of LFA-1 to the ICAM in the presence and absence of a test compound, (ii) identifying as a negative regulator the compound which decreases LFA-1 binding to the ICAM and which competes with (2-isopropyl-phenyl)[2-nitro-4-(E-((4-acetyl-piperazin-1-yl)carbonyl)ethenyl)phenyl]sulfide for binding to LFA-1 α_L polypeptide. Alternatively, the negative regulator competes with 4-amino-2-chlorophenyl-(1'-chloro-2-naphthylphenyl)-sulfide for binding to LFA-1 α_L polypeptide.

In addition, the regulatory site is defined as the site binding site for a negative regulatory that competes for binding to LFA-1 with one of 3-chloro-4-(1-chloro-naphthalen-2-ylsulfanyl)-phenylamine, 2-iso-propylphenyl)[2-nitro-4-(E-((4-acetyl-piperazin-1-yl)carbonyl)ethenyl)phenyl]sulfide, (4-methylphenyl)[2-nitro-4-(E-((4-acetyl-piperazin-1-yl)carbonyl)ethenyl)phenyl]sulfide, 3-chloro-4-(2-chloro-4-(N,N-dimethylamino)-phenylsulfanyl)-phenylamine, [3-chloro-4-(4-isopropylphenyl-sulfanyl)phenyl]methylamine, (2,4,-dichlorophenyl)[2-chloro-4-(E-((3-(1-pyrrolidin-2-onyl)propylamino)carbonyl)ethenyl)phenyl]sulfide, (2-methylphenyl)[2-nitro-4-(E-((4-acetyl-piperazin-1-yl)carbonyl)ethenyl)phenyl]sulfide, (2-formylphenyl)[2-nitro-4-E-((4-acetyl-piperazin-1-yl)carbonyl)ethenyl)phenyl]sulfide, and 1-[4-(2-isopropyl-phenylsulfanyl)-piperidin-1-yl]ethanone.

The invention also provides methods to identify candidate compounds particularly useful as negative regulators of LFA-1 binding to an ICAM that binds LFA-1 comprising the steps of (i) contacting LFA-1 with (2-isopropyl-phenyl)[2-nitro-4-(E-((4-acetyl-piperazin-1-yl)carbonyl)ethenyl)phenyl]sulfide in the presence and absence of a compound, and (ii) identifying the compound as a putative negative regulator wherein the compound competes with (2-isopropyl-phenyl)[2-nitro-4-(E-((4-

acetyl(piperazin-1-yl)carbonyl)ethenyl)phenyl]sulfide for binding to the LFA-1 α_L polypeptide. The invention therefore provides a method to screen for candidate negative regulators and/or to confirm the mode of action of compounds that decrease LFA-1 binding to an ICAM.

5 The methods of the invention to identify negative regulators are particularly amenable to the various high throughput screening techniques known in the art. There are a number of different libraries used for the identification of small molecule modulators in these screening techniques of the invention, including, (1) chemical libraries, (2) natural product libraries, and (3) combinatorial libraries

10 comprised of random peptides, oligonucleotides or organic molecules. Chemical libraries consist of structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening. Natural product libraries are collections of microorganisms, animals, plants, or marine organisms which are used to create mixtures for screening by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of plants or marine

15 organisms. Natural product libraries include polyketides, non-ribosomal peptides, and variants (non-naturally occurring) thereof. For a review, see *Science* 282:63-68 (1998). Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds as a mixture. They are relatively easy to prepare by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see

20 Myers, *Curr. Opin. Biotechnol.* 8:701-707 (1997). Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to modulate activity.

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In high throughput screening methods embraced by the invention, robotic methods are contemplated wherein libraries comprising tens to hundreds of thousands of compounds can be rapidly and efficiently screened.

The invention further provides novel compounds identified as negative regulators in methods of the invention. Negative regulators of the invention are compounds that decrease LFA-1 binding to an ICAM (as compared to binding in the absence of the compound) and compete with (2-isopropyl-phenyl)[2-nitro-4-(E-((4-acetyl-piperazin-1-yl)carbonyl)ethenyl)phenyl]sulfide for binding to the α_L polypeptide of LFA-1. Presently preferred inhibitors are substituted diaryl sulfides. Exemplary compounds include those as described in co-pending U.S. patent applications entitled "Cell Adhesion-Inhibiting Antiinflammatory and Immune Suppressive Compounds" filed April 2, 1999, attorney docket number 6446.US.Z3, Serial Number 09/286,645, incorporated herein by reference in its entirety, and "Inhibitors of LFA-1 Binding to ICAMs and Uses Thereof" filed April 2, 1999, attorney docket number 27866/35374, USSN 09/285,325, incorporated herein by reference in its entirety.

The invention also provides compositions comprising negative regulators of the invention, and preferably pharmaceutical compositions further comprising a pharmaceutically acceptable diluent or carrier. Pharmaceutical compositions are particularly useful for treatment of a variety of pathological disorders in humans or other animals, e.g., disorders amenable to animal models as described above.

The invention further provides use of a negative regulator identified by a method of the invention in the production of a medicament to ameliorate pathologies arising from LFA-1 binding to an ICAM that binds LFA-1.

The invention also provides kits to identify inhibitors of LFA-1 binding to an ICAM that binds LFA-1, comprising one or more of a purified and isolated LFA-1 polypeptide, a purified and isolated ICAM polypeptide that binds LFA-1, cells expressing LFA-1, and cells expressing the ICAM. Appropriate control reagents and buffers are contemplated in kits of the invention.

The present invention is illustrated by the following examples. Example 1 describes a high throughput assay to identify inhibitors of LFA-1 binding to full length ICAM-1. Example 2 relates to identification of LFA-1 residues that

participate in antagonist binding. Example 3 describes production of an antibody that activates LFA-1. Example 4 describes identification of an ICAM-1 binding site on LFA-1.

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Example 1 High Throughput Screening for LFA-1/ICAM-1 Binding Inhibitors

In an effort to identify inhibitors of LFA-1/ICAM-1 binding, a high throughput screening (HTS) assay was designed to efficiently screen large numbers of chemical compounds in a proprietary library as follows.

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Preliminary experiments were carried out in order to define the linear range of LFA-1/ICAM-1 interaction. Recombinant ICAM-1/IgG1 fusion protein (comprising full length ICAM-1) was prepared as described in U.S. Patent Nos. 5,770,686, 5,837,478, and 5,869,262, each of which is incorporated herein by reference. The extracellular domain of ICAM-1 was subcloned into plasmid pDC1 by standard methods to generate an expression construct encoding a chimeric protein containing the ICAM-1 extracellular domain fused to the Fc region of the heavy chain of human IgG1 just upstream of the hinge. The protein was expressed in CHO cells and purified using protein A Sepharose[®]. The fusion protein was biotinylated using a kit obtained from Pierce Chemical (Rockford, IL). Biotinylated protein

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(BioIgICAM-1) concentration was determined by measuring absorbance at 280 nm, and serial dilutions were prepared to give a final concentration range of 50 µg/ml to 0.008 µg/ml. Titration of BioIgICAM-1 was carried out with the protein first aliquoted into wells on an assay plate. Recombinant LFA-1 was added to each well at the same concentration and the experiment (as described below) was carried out to completion. The amount of binding was determined for each well, and from a subsequent plot of the results, a single concentration of BioIgICAM-1 was selected for subsequent experiments. In a similar manner, LFA-1 was titrated using the BioIgICAM-1 concentration selected as described above.

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On day 1 of the HTS procedure, the capture antibody, *i.e.*, a non-blocking anti-LFA-1 monoclonal antibody (TS2/4.1; ATCC #HB244), was diluted in plate coating buffer (50 mM sodium carbonate/bicarbonate, 0.05% ProClin[®] 300, pH 9.6) to a final concentration of 2 µg/ml. Immulon[®] 4 (Dynex

Technologies, Chantilly, VA) plate wells were coated with 100 µl diluted antibody solution per well, and incubation was carried out overnight at 4°C. On day 2, the plates were warmed to room temperature and washed two times with wash buffer (calcium- and magnesium-free phosphate buffered saline, CMF-PBS) with 0.05% Tween[®]-20). To each well, 200 µl of blocking solution (5% fish skin gelatin in CMF-PBS with 0.05% ProClin[®] 300) was added, and the blocking incubation was carried out at room temperature for 30 min. The blocking solution was removed by aspiration, and the plates were not washed. LFA-1 was diluted to a final concentration of 1 µg/ml in assay buffer (1% fish skin gelatin and 2 mM MgCl₂ in CMF-PBS), and 100 µl was added to each well. Incubation was carried out for one hour, and the plates were washed two times with wash buffer.

A 2X stock solution of BioIgICAM-1 was prepared containing 0.1 µg/ml BioIgICAM-1 and 4 µM crystal violet (an activator of LFA-1/ICAM-1 binding) in Assay Buffer (EG&G Wallac, Gaithersburg, MD). Diluted aliquots (50 µl) of pooled chemicals (22 compounds/pool) from the chemical library were added to the wells, followed by addition of 50 µl of the 2X stock of BioIgICAM-1 to provide a final assay volume of 100 µl (containing 2% DMSO). The plates were incubated for one hour at room temperature and washed once with wash buffer. Europium-labeled streptavidin (Eu-SA; #1244-360, EG&G Wallac) was diluted 1:500 in Assay Buffer, 100 µl of the diluted Eu-SA was added to each well, and the plates were incubated at room temperature for one hour.

Plates were washed eight times with wash buffer, 100 µl of DELFIA[®] enhancement solution (EG&G Wallac) diluted 1:2, was added to each well, and the plates were shaken for five minutes using a Wallac shaker at fast speed. Plates were read using a Wallac DELFIA[®] fluorescence reader (fluorimeter). Controls included both positive and negative wells and 50% binding wells established using blocking antibodies, *i.e.*, anti-LFA-1 monoclonal antibody (TS1/22.1, ATCC #HB202) or an anti-ICAM-1 monoclonal antibody. Chemical pools in wells showing 50% or greater inhibition of LFA-1 binding to ICAM-1 were identified and the experiment was repeated using individual chemicals from those pools. Inhibitors of LFA-1/ICAM-1 binding were identified, and a further screen was performed to determine dose

dependence of the inhibitory activity. Further study of selected compounds was carried out using biochemical and cellular assay techniques.

The HTS assay identified more than 40 compounds as hits demonstrating potency in inhibiting LFA-1/ICAM-1 interaction. Of these many, 5 compounds exhibited a diaryl sulfide structure, thereby identifying these compounds as a class of LFA-1/ICAM-1 binding inhibitors.

Example 2
Identification of an LFA-1 Regulatory Binding Site

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A. LFA-1 Antagonist Binding to the LFA-1 I domain

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Nuclear magnetic resonance (NMR) spectroscopy has proven to be a useful technique to detect small molecule binding to proteins. This technique for screening, or establishing the structure activity relationship (SAR) by NMR [Shuker, *et al., Science 274:1531-1534 (1996), incorporated herein by reference], has been successful to identify drug leads against several proteins [WO 97/18471, published May 22, 1997 and WO 97/18469, published May 22, 1997, both of which are incorporated herein by reference]. This technique relies on detecting chemical shifts of amide proton and nitrogen atoms resulting from changes in the chemical environment of the peptide backbone, such as those that occur upon ligand binding. Based on the technique's sensitivity, experiments were designed to evaluate binding of small molecule antagonists to LFA-1 in order to understand the structural basis for chemical inhibition of LFA-1 binding to ICAM-1.*

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Intact LFA-1 is too large to study by NMR spectroscopy. However, evidence indicates that the α_L chain I domain of LFA-1 is largely responsible for ICAM-1 binding, and recombinant I domain polypeptides can compete with intact LFA-1 for ICAM-1 binding. The approximately 200 amino acid I domain region was therefore subcloned, and the recombinant polypeptide was used in NMR experiments to assess whether antagonists of LFA-mediated adhesion interact with the I domain.

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The I domain polypeptide corresponding to residues 127-309 in SEQ ID NO: 1 was isotopically labeled in *E. coli* and purified. The pET15b plasmids encoding residues 127-310, 127-309, or 127-305 of SEQ ID NO: 2 were prepared by

PCR amplification of the respective sequences using the human LFA-1 gene as a template and cloned using standard techniques. Each expression plasmid was checked by sequencing.

For NMR experiments, uniformly ^{15}N - or ^{15}N -, ^{13}C -labeled protein was prepared by growing the *E. coli* strain BL21 (DE3) overexpressing the I domain of LFA-1 on M9 medium containing $^{15}\text{NH}_4\text{Cl}$ with or without [U- ^{13}C]-glucose. In addition, [^{15}N , ^2H]-labeled proteins, with [^{13}C]-labeled methyl protons in valine and leucine, were prepared to facilitate the interpretation of ^{13}C NOESY experiments [Gardner and Kay, *J. Am. Chem. Sci.* 119:7599 (1997)]. The recombinant I domain was purified using nickel affinity resin according to the manufacturer's suggested protocol. The NMR samples contained 0.8 mM protein, 100 mM sodium phosphate, pH 7.2, in $\text{H}_2\text{O}/\text{D}_2\text{O}$ (9:1) or 99.9% D_2O .

All NMR spectra were acquired at 30°C on Bruker DRX500 or DRX600 NMR spectrometers. Backbone resonances were assigned using the HNCA, HN(CO)CA, HN(CA)CB, HN(COCA)CB, HNCO and HN(CA)CO triple resonance experiments using uniformly ^{15}N , ^{13}C labeled protein. Sidechain assignments were made using the HACACO, HBHA(CO)NH, ^{15}N Edited TOCSY and the HCCH-TOCSY three dimensional experiments. Distance restraints were obtained from ^{13}C -resolved 3D NOESY and ^{13}C edited-filtered NOESY experiments.

Models for the bound compounds were generated with a simulated annealing protocol using the program XPLOR. The docking calculations were performed using the NMR derived distance constraints. The starting protein coordinates in these calculations were derived from the x-ray crystal structure [Qu and Leahy, *Proc. Natl. Acad. Sci. (USA)* 92:10277-10281 (1995)]. Starting structures for the compound were generated randomly. The backbone atoms of the protein were fixed in the docking calculations.

The two dimensional heteronuclear single quantum correlation (HSQC) spectra of the ^{15}N -labeled I domain was indicative of a folded structure. Addition of (2-isopropyl-phenyl)[2-nitro-4-(E-((4-acetylpirazin-1-yl)carbonyl)ethenyl)phenyl]sulfide induced multiple chemical shift changes in the

LFA-1 domain spectrum thereby confirming that the I domain of LFA-1 binds to this antagonist.

B. Binding Interface of Small Molecule Ligand with LFA-1 I domain

To identify the amino acids whose chemical shifts were perturbed by the antagonist, *i.e.*, to map the negative regulator binding site, backbone and side chain resonance assignments of the protein were made using standard heteronuclear NMR experiments. The secondary structure of truncated LFA-1 I-domain protein was compared to that of the x-ray crystal structure of the I domain in intact LFA-1 [Qu and Leahy, *supra*], using both nuclear Overhauser effects (NOE) and backbone chemical shifts. Data indicated that the secondary structure of the I domain in the truncated protein was identical to that found in the previously defined LFA-1 crystal structure. As a result, the antagonist-induced chemical shift changes, as determined by NMR, could then be reliably mapped onto the three-dimensional structure of the I domain, as determined by x-ray crystallography.

In these studies, the largest chemical shift changes occurred for residues that lined a cleft between the carboxy terminal helix of the I domain and central beta sheets. Residues adjacent the metal binding site (MIDAS) showed no shift upon negative regulator binding.

More detailed analysis of (2-isopropyl-phenyl)[2-nitro-4-(E-((4-acetyl13C edited and ¹³C edited-filtered NOE experiments were used to identify NOEs between the negative regulator and protein.

Thirty-nine regulatory site contacts were identified and used to dock the negative regulator into the protein. The inter-protein NOEs that were observed in the complex are similar to those predicted by the crystal structure for the I domain.

Based on this observation, the negative regulator/free crystal structure coordinates were used as the starting conformation for the protein in a proposed model of the protein/regulator complex.

Negative regulators were docked using the NOE constraints and the program XPLOR. In the docking calculations, the protein backbone was kept rigid, but amino acid sidechains of the protein were allowed to relax to accommodate the ligand. Only minor changes in protein conformation were necessary to dock the regulator. In all of the docking calculations, the negative regulator was found to lie in the cleft between beta sheet 5 and the carboxy terminal helix, alpha 7 in the I domain, in agreement with the model based on chemical shift changes. The top of the binding pocket is formed from the loop connecting alpha helix 7 to beta sheet 5. Negative regulator ring A is positioned to the top part of the cleft by NOE constraints to Ile²⁵⁹ and Leu²⁹⁸ while ring B makes contact to the middle of the cleft with NOEs to Ile²³⁵, Val¹⁵⁷, Leu¹⁶¹ and Ile³⁰⁶. The contacts Val¹⁵⁷ and Leu¹⁶¹ on the helix-5 indicate how deep into the protein pocket ring B sits in the complex. Residue Ile²³⁵ is positioned near the center of the negative regulator and shows large chemical shifts upon regulator binding.

The number of constraints obtained was not sufficient to generate an exhaustively detailed model of the complex. However, the constraints identified unambiguously place the negative regulator binding site in this cleft of the protein. The low number of constraints was due to low sensitivity of NMR signals from residue in the binding pocket that resulted from chemical exchange broadening. Chemical exchange broadening is often indicative of slow motions between different environments. This is generally observed for loose binding of compounds that do not bind in a single conformation. Indeed, some of the constraints observed between the negative regulator and protein were not consistent with a single conformation. For instance, in the docking calculations, two families of possible conformations were found, one pointing toward beta sheet 5 and Ile²⁵⁹, and another with ring A pointing toward alpha helix 7 and residue Leu²⁹⁸.

Results indicated that the protein binding pocket is lined predominantly by hydrophobic Leu/Val/Ile residues. The hydrophobic pocket is,

however, ringed by several hydrophilic groups of lysine and glutamic acid residues. In the ligand-free crystal structure, these hydrophilic groups shield the hydrophobic binding pocket from solvent, possibly by forming salt bridges. In the model for the complex, these hydrophilic side chains move to accommodate the negative regulator.

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Example 3

Production of Activating Monoclonal Antibody 240Q

Female BALB/c mice were immunized with purified recombinant

α_d /CD18 (described in U.S. Patent 5,837,478, issued November 17, 1998, and incorporated herein by reference). The protein was captured from CHO cell supernatant with a CD18-specific antibody captured on protein A Sepharose[®] beads. Column material (including beads and capture antibody) was injected with incomplete Freund's adjuvant. Four immunizations over a seven month period were performed before animal #2480 was sacrificed for harvest and fusion of the spleen.

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Hybridomas were screened by ELISA for production of IgG by standard protocols. A secondary ELISA screen was performed to identify hybridoma supernatant reactive with either the integrin α or β chain. Briefly, plates were coated in standard buffer with 100 ng/ml of the F(ab')₂ fragment of the CD18-specific antibody, 195N. After a blocking step, CHO cells supernatants containing either soluble α_d /CD18 or CD11a/CD18 were added to the wells and capture of integrins was allowed to continue for four hours at 37°C. Hybridoma supernatants were incubated with bound integrin, after which bound mouse IgG was detected with a horseradish peroxidase-conjugated anti-mouse Fc-specific polyclonal antibody. Hybridomas that reacted with both α_d /CD18 and CD11a/CD18 were presumed to recognize either the common β chain or the leucine zipper region of the recombinant molecule. Supernatants were tested by flow cytometry for recognition of native α_d on α_d -transfected JY cells and HL60 cells. Hybridomas that reacted with neither were presumed to be reactive with the leucine zipper peptides.

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Thirty five hybridomas were identified as CD18-specific in the

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secondary assay. A tertiary screen was performed to determine whether the antibodies exhibited any function in an adhesion assay measuring the interaction between peripheral blood lymphocytes (PBL) and ICAM-1. Briefly, PBL were isolated from

heparin-treated whole blood by centrifugation on a Ficoll® gradient. Monocytes and activated lymphocytes were removed by adherence on plastic. Non-adherent cells were treated with hybridoma supernatants or control antibodies for one hour on ice. As a positive control for activation, phorbol myristate acetate (PMA) was used to stimulate a subset of PBL. Cells were washed once and incubated with ICAM-1 immobilized on microtiter plates. After 45 min at 37°C, bound cells were crosslinked for 12 hr using 2.5% (final concentration) glutaraldehyde. Plates were washed in distilled water and stained with 0.5% (final concentration) crystal violet. Following extensive washing with distilled water, destaining was performed using 66% absolute ethanol. Plates were read on a Beckman ELISA reader with a test filter of 570 nm. Six hybridomas were identified that produced an anti-CD18 monoclonal antibody capable of enhancing PBL binding to ICAM-1 at the same level as the PMA control (three- to four-fold over unstimulated cells). The hybridomas were cloned in successive rounds using a modified limiting dilution method. Five clones survived the cloning process and were retested in the PBL assay and with B and T cells. The antibody 240Q was developed further since it appeared to be more effective at cell stimulation.

Specificity of 240Q was assessed by immunoprecipitation experiments. Biotinylated lysates of HL60 cells, positive for expression of all β_2 integrins, were treated with anti-CD18 antibodies 23I11B, 195N, TS1.18 or with 240Q. Antibody/antigen complexes were isolated with an anti-mouse Ig conjugated to protein A Sepharose® matrix. After resolution of protein by SDS-PAGE, biotinylated species were visualized by detection with streptavidin-HRP and developed with a chemiluminescent reagent (Amersham). Antibody 240Q precipitated the identical series of proteins as the known CD18 antibodies. The bands represented known molecular weight proteins for all of the leukointegrin α chains and the CD18 β chain. Extensive immunocytochemical analyses comparing 240Q staining with that of the other anti-CD18 antibodies indicated that 240Q recognized the β chain.

Further evidence that 240Q recognized the β chain (and not a shared epitope on the α chain) was derived from additional immunoprecipitation experiments. It is known that expression of integrins lacking the transmembrane and

cytoplasmic domains results in secretion of large amounts of the free β chain. While the anti-CD18 antibody 195N will bind to and precipitate free β chain, the 23I11B antibody will recognize β chain only in the context of a heterodimer.

Immunoprecipitation of soluble α_6 /CD18LZ (leucine zipper) protein from CHO supernatants yields protein that, on SDS-PAGE, is predominantly β chain, with non-stoichiometric amounts of the appropriate alpha chain. In these experiments, the affinity resin is not washed, so disruption of the bound heterodimer would not be expected to affect results.

Several integrin-specific monoclonal antibodies were biotinylated and used in flow cytometry designed to map the 240Q binding site on a coarse level. Cells were incubated with a biotinylated antibody and a different, unlabeled antibody at the same time, and it was determined whether the unlabeled antibody can compete with the labeled antibody. The untreated control consisted of cells stained with the biotinylated antibody alone.

A preliminary experiment was performed to titrate single antibodies with HUT78 (CD11a/CD18 $^+$ T cell line) and HL60 (CD11a $^+$, CD11b $^+$, CD11c $^+$ myeloid lineage cell line). Biotinylated antibodies were incubated with both cell types at 0.3, 1.0, 3.0, and 10 μ g/ml. Biotinylated antibody was detected with both streptavidin-FITC (to determine whether biotinylation was successful) and anti-mouse Ig/FITC (to determine whether biotinylated antibodies were still functional and binding at equivalent levels). Staining with 240Q with the streptavidin-FITC detection method was only 25% that of the CD18-specific antibody 23I11B at any given concentration. The difference was more dramatic with the anti-mouse FITC detection. Affinity differences would not be expected to account for these results, since transformants stained equally well with both antibodies.

This result implied that 240Q recognizes a specific subset of CD18 molecules on the cell surface, a finding that correlated with previous staining of COS transfecteds. Another possibility is that the antibody recognized a particular molecular conformation achieved temporally at only 25% of the time.

In the cross-competition experiments, there appeared to be no overlap between 240Q and any other integrin α or β chain-specific antibodies. This finding

was confirmed by ELISAs with captured recombinant LFA-1 and Mac-1 protein. In these assays, the unlabeled antibody was used to capture the protein and the labeled antibody was used to detect it. Failure of the labeled antibody to bind would indicate that the binding site was occupied by the capture antibody. While 240Q capture blocked binding of biotinylated 240Q, it did not block binding with any other antibody. Capture by CD11a, CD11b, or other CD18 antibodies did not prevent detection by biotinylated 240Q. There was no difference between the ability of 240Q and other CD18-specific antibodies to recognize recombinant CD18 integrins.

Treatment of immobilized recombinant LFA-1 with either 240Q or manganese did not enhance ICAM-1 binding, implying that the recombinant integrin was in a constitutively activated conformation.

Based on the observation that 240Q treatment of cells in the cross-blocking experiments caused aggregation, an aggregation assay was run with JY, Jurkat, and HL60 cells. Cells were plated in culture medium and treated with concentrations of 240Q or 195N ranging from 0.2 to 10 µg/ml. After a 30 minute incubation at 37°C, wells were photographed. Antibody 240Q at concentrations from 0.5 - 10 µg/ml appeared to induce substantial aggregation. Antibody 195N did not induce the aggregate phenotype. It was not apparent whether this behavior was due to integrin-CAM interactions or an indirect induction of other adhesive pathways.

The integrin-activation function of 240Q was further characterized in binding experiments using the TACO cell line. These cells were isolated from a patient diagnosed with a subtype of leukocyte adhesion deficiency (LAD). The subtype is characterized by normal surface expression of LFA-1 on lymphocytes, but the inability of LFA-1 to bind ICAM-1. The functional phenotype is not recognized by phorbol myristate acetate (PMA). Treatment of the cells with the antibody 240Q rescued homotypic aggregation, which was determined to be ICAM-1-dependent using an ICAM-1-specific antibody. When subsaturating amounts of the antibody F(ab')₂ fragment were used to treat the cells, aggregation did not occur and the 240Q-treated cells were capable of recognizing ICAM-1/Fc protein immobilized on microtiter plates. Cells which were treated with the anti-CD18 antibody and either no

240Q antibody or PMA did not bind immobilized ICAM-1/Fc. This data indicated that the mechanism of integrin activation by PMA and 240Q is distinct.

Example 4 ICAM-1 Binding Site

A. Production and Purification of Recombinant Human ICAM-1 Domains 1 and 2

Domains 1 and 2 of human ICAM-1 were amplified by PCR by standard methods using primers d1/HindIII and d2/XbaI and an ICAM-1 cDNA as template.

d1/HindIII	CCCAAGCTTCCGCCGCCACCATGGCTCCCAGCAG	SEQ ID NO: 3
d2/XbaI	TGCTCTAGACTGGTGATGGTGATGGT- GATGAAAGGTCTGGAGCTGGTAGGGG	SEQ ID NO: 4

The amplification product was digested with *Hind*III and *Xba*I and gel purified. The purified fragment was used in a three-way ligation including ICAM-1 domains 1 and 2 (the *Hind*III/*Xba*I fragment), pDEF17 previously digested with *Xba*I and *Not*I, and pDEF17 previously digested with *Not*I and *Hind*III, and the resulting plasmid, pDEF17/ICAM-1 domains 1 and 2, was sequenced. For expression, the plasmid was transformed into CHO cells by standard methods.

A 70 ml immunoaffinity column was created by coupling 2 mg of a non-blocking anti-ICAM-1 18E3D monoclonal antibody per ml of activated CNBr-Sepharose[®] according to the manufacturer's suggested protocol. The column was equilibrated with 20 mM Tris/150 mM NaCl at pH 7.5. Approximately 2.5 liters of culture supernatant from CHO cells secreting recombinant human ICAM-1 domains 1 and 2 was applied to the column overnight at 4°C. The following morning, the column was washed to baseline protein elution with equilibration buffer. The column was eluted with 2 M KSCN, pH 8.0, and fractions were analyzed by SDS-PAGE under reducing conditions. Samples containing pure ICAM-1 domains 1 and 2 were pooled, the buffer was exchanged into 20 mM Tris/150 mM NaCl/pH 7.5,

and the protein was concentrated ten-fold. Concentration of the protein was determined by absorption at 280 nm using an extinction coefficient of 1.0 AU/1.4 mg of ICAM-1 domain 1 and 2. The purification process and analysis was repeated using the same column and an additional 2.5 liters of CHO culture supernatant. The two 5 pools were combined and filtered.

B. ICAM-1 Binding Interface on the LFA-1 I-Domain

Residues that are important for ICAM-1 binding to the LFA-1 I domain have previously been identified using mutational studies and residues that 10 form the MIDAS region of the I domain have been shown to be important for binding by this approach. Other LFA-1 regions have been investigated using chimeric proteins comprising human and mouse I domains [Huang and Springer, *J. Biol. Chem.* 270:19008-19016 (1995)]. Because many of the residues in the LFA-1 ligand binding site important for ICAM-1 binding are either identical (Tyr³⁰⁷, Lys³⁰¹, Lys²⁸⁷) or highly 15 conserved (human Lys³⁰⁵, Lys³⁰⁴ - mouse Arg³⁰⁵, Arg³⁰⁴) between mouse and human, chimeric protein studies were unable to specifically identify necessary binding residues. Chemical shift changes that occur upon binding provides a sensitive way to map binding sites. ¹H-¹³C HSQC and ¹H-¹⁵N HSQC spectra of the I domains of LFA-1 in the presence and absence of ICAM-1 were used to identify residues affected 20 by ICAM-1 domains 1 and 2 fragment binding using NMR techniques as generally described above.

The complex was found to be in slow exchange on the NMR timescale, indicating binding much tighter than 10 μM. Many residues whose NMR signals show the largest changes upon binding were found on the surface of the I 25 domain. In addition, residues near the MIDAS motif and alpha helix 7 of the small molecule ligand binding site were most affected by ICAM-1 binding. These data indicate that the MIDAS motif and alpha helix 7 participate in ICAM-1 binding, either directly by binding the ligand, or indirectly by mediating a conformational change in the I domain. Furthermore, the involvement of the α helix 7 in ICAM-1 30 binding provides a rationale for how small molecules that bind to this region of the I domain disrupt LFA-mediated adhesion.

C. Functionally Important Residues in the Ligand Binding Pocket

In an attempt to identify functional I domain residues in and around the site of compound binding, amino acid substitution mutants were generated and tested for the ability to bind ICAM-1. Amino acids most affected in NMR by compound binding and whose side chains are directed toward the surface of the I domain were substituted with alanine. In addition, Asp¹³⁷, a residue located within and essential to a functional MIDAS and ICAM-1 binding site, was substituted with alanine. The various I domain mutants were expressed in COS cells and cell adhesion to ICAM-1 was determined in the presence of a CD18 monoclonal antibody, 240Q, that induces high avidity binding.

1. Generation of the mutations in the CD11a I domain:

Twenty-five individual mutations in the LFA-1 α polypeptide (CD11a) were generated. Each mutation was prepared using Stratagene's QuikChange™ Site-Directed Mutagenesis Kit (Stratagene, La Jolla, CA). Briefly, two primers were synthesized that introduced a specific mutation in the amplification product. Primers utilized are set out below, with only the sense primer shown.

D137A/S: SEQ ID NO: 5

20 CTGGTATTCTGTTGCGGGTCGATGAGCTTG

V157A/S: SEQ ID NO: 6

GACTTCATGAAGGATGCGATGAAGAAACTCAGC

K160A/S: SEQ ID NO: 7

GAAGGATGTGATGAAGGCGCTCAGCAACACTTGC

25 E218A/S: SEQ ID NO: 8

CAATTATGTCGCGACAGCGGTGTTCCGGGAGGAG

T231A/S: SEQ ID NO: 9

GCCCCGCCAGATGCCCGAAAGTGCTTATCATC

K232A/S: SEQ ID NO: 10

CGGCCAGATGCCACCGCGGTGCTTATCATCATC

I235A/S: SEQ ID NO: 11
GCCACCAAAGTGCTTGCATCATCACGGATGGG

D253A/S: SEQ ID NO: 12
CATCGATGCGGCCAAAGCGATCATCCGCTACATC

5 I255A/S: SEQ ID NO: 13
GCGGCCAAAGACATCGCGCTACATCATCGGG

K280A/S: SEQ ID NO: 14
CACAAATTGCATCAGCGCCCGCGAGCGAGTTG

S283A/S: SEQ ID NO: 15
10 GCATCAAAACCGCGGGAGTTGTGAAAATTTC

E284A/S: SEQ ID NO: 16
CAAAACCCCGAGCGCGTTGTGAAAATTCTG

K287A/S: SEQ ID NO: 17
GCGAGCGAGTTGTGGCGATTCTGGACACATTG

15 K294A/S: SEQ ID NO: 18
CTGGACACATTGAGGCGCTGAAAGATCTATTTC

E301A/S: SEQ ID NO: 19
GAAAGATCTATTCACTGCGCTGCAGAAGAAGATC

Q303A/S: SEQ ID NO: 20
20 CTATTCACTGAGCTGGCGAAGAAGATCTATGTC

K304A/S: SEQ ID NO: 21
TTCACTGAGCTGCAGGCGAAGATCTATGTCATTG

K305A/S: SEQ ID NO: 22
CACTGAGCTGCAGAAGGCGATCTATGTCATTGAG

25 I306A/S: SEQ ID NO: 23
GAGCTGCAGAAGAAGGCGTATGTCATTGAGGGC

Y307A/S: SEQ ID NO: 24
30 Control mutants included the following, wherein amino acid changes were introduced
in regions reported by others to be involved in ICAM-1 binding.
CTGCAGAAGAAGATCGCGGTATTGAGGGCACA

T243A/S: SEQ ID NO: 25
ACGGATGGGGAGGCCGCGGACAGTGGAACATC

S245A/S: SEQ ID NO: 26
GGGGAGGCCACTGACGCAGAACATCGATGC

5 N247A/S: SEQ ID NO: 27
GCCACTGACAGTGGCGCGATCGATGCCAAAG

D249A/S: SEQ ID NO: 28
GACAGTGGAACATCGCGCGCCAAAGACATC

K252A/S: SEQ ID NO: 29
10 CAACATCGATGCCCGCGAACATCATCCGCTAC

The primers were used in two PCR reactions, one with full-length CD11a (residues 1-1170) in plasmid pDC1 as template and the other with CD11a I domain (residues 152-334) in plasmid pET15b as template. PCR reaction conditions varied depending on

15 the melting temperature (T_m) of the primers. Details of the reaction for each mutation are described below. The general format was as follows: one cycle at 95°C for 30 seconds followed by 16 cycles of: 95°C for 30 seconds, 55°C for one minute, and 68°C for 20 minutes. After PCR, template DNA was digested with *Dpn*I at 37°C for one hour and the remaining amplified DNA was used to transform supercompetent *E.*

20 *coli* XL1 Blue (Stratagene) according to the manufacturer's suggested protocol.

Selected colonies were grown in liquid culture and plasmid DNA was isolated and sequenced. For the full-length mutants, a 1.8 kb *Hind*III/*Eco*RI fragment containing the 5' half of the gene was isolated and subcloned into the parental vector. Subclones were sequenced to verify the integrity of the junctions and the presence of the

25 mutation.

2. PCR Conditions

Mutations V157A, E218A, T231A, I235A, I255A, E284A, K287A, K294A, K305A were generated in PCR including a 45°C annealing step and a 58°C extension step. In generating these mutations, extension times for the full length sequence in pDC1 was 20 minutes and 15 minutes for I domain in pET15b.

For mutations D137A, K160A, K232A, K280A, S283A, E301A, Q303A, K304A and I306A, the same temperatures as described above were used, but with both templates, the extension time for both templates was 20 minutes. For mutants Y307A and D253A, an extension step of 25 minutes was used.

5 For mutants T243A, S245A, N247A, D249A and K252A, the annealing step was carried out at 45°C, and extension was carried out at 60°C for 20 minutes. For mutant S245A, PCR included 18 cycles rather than 16 cycles.

3. COS Cell Transfections

10 On day 1, COS cells were seeded at 1.6×10^6 cells per 10 cm plate in DMEM 10% FBS (growth media). After 18 to 24 hr, cells were transfected as follows. Seven μ g each of CD18/pDC1 and CD11a/pDC1 plasmid DNA was added to three ml OPTI MEM media and 49 μ l Lipofectamine was added to another three ml of the same media. The two resulting solutions were mixed, inverted five times, incubated
15 at room temperature for 30 min, and diluted by addition of 6.1 ml OPTI MEM. Cells were washed once with OPTI MEM and the DNA/Lipofectamine mixture was added. Cells in the mixture were incubated at 37°C in CO₂ for six hours. Media containing the plasmid DNA was removed and replaced with growth media. Cells were grown overnight and media was removed and replaced. After overnight growth, cells were
20 split 1:2 and grown overnight again. Cells were removed from the plate with Versene, collected by centrifugation, resuspended in adhesion buffer containing (RPMI containing 5% inactivated FBS), and counted. Cells were then used for adhesion assays and for fluorescence activated cell sorting (FACS) staining and analysis.

25 4. Adhesion Assay

Adhesion assays were performed in 96-well Easy Wash plates (Corning, Corning NY) using a modification of a previously reported procedure [Sadhu, *et al.*, *Cell. Adhes. Commun.* 2:429-440 (1994)]. Each well was coated overnight at 4°C with (i) 50 μ l of ICAM-1/Fc (5 μ g/ml), (ii) anti-CD18 monoclonal antibody TS1/18 [Sanchez-Madrid, *et al.*, *Proc. Natl. Acad. Sci. (USA)* 79:7489-7493 (1982); Weber, *et al.*, *J. Immunol.* 159:3968-3975 (1997); Lu, *et al.*, *J. Immunol.*

159:268-278 (1997)] at 5 µg/ml together with anti-CD11a monoclonal antibody TS1/22 at 5 µg/ml in 50 mM bicarbonate buffer, pH 9.6, or (iii) buffer alone. Plates were washed twice with 200 µl per well D-PBS and blocked with 1% BSA (100 µl/well) in D-PBS for one hour at room temperature. Wells were rinsed once with 5 100 µl adhesion buffer (described above) and 100 µl adhesion buffer was then added to each well. Adhesion buffer (100 µl) with or without blocking antibody TS1/22 at 20 µg/ml was added to each well. COS transfectants (100 µl, approximately 0.75 x 10⁶ cells/ml) expressing the heterodimer (with or without a mutation) in adhesion buffer, with or without activating antibody 240Q (10 µg/ml) was added to each well 10 and the plates incubated at 37°C for 15 to 20 min. Adherent cells were fixed by addition of 50 µl/well 14% glutaraldehyde in D-PBS and incubated at room temperature for 1.5 hr. The plates were washed with dH₂O and stained with 100 µl/well 0.5% crystal violet in 10% ethanol for five minutes at room temperature. Plates were washed in several changes of dH₂O. After washing, 70% ethanol was 15 added, and adherent cells were quantitated by determining absorbance at 570 nm and 410 nm using a SPECTRAmax® 250 microplate spectrophotometer system (Molecular Devices, Sunnyvale, CA). Percentage of cells binding was calculated using the formula:

$$20 \quad \% \text{ cells binding} = \frac{A_{570} - A_{410}(\text{binding to ICAM-1})}{A_{570} - A_{410}(\text{binding to CD18 + CD11a antibody})} \times 100$$

25 Data were normalized using the formula:

$$\% \text{ wildtype binding} = \frac{(\% \text{ mutant cell binding})}{(\% \text{ wildtype cells binding})} \times 100$$

5. FACS Staining

30 FACS staining was carried out in a 96 well plate. Each transfectant was stained with an antibody to CD18 (TS1/18), an antibody to CD11a (TS1/22), and an activating antibody to CD18 (240Q). Controls included unstained cells, cells

stained with secondary antibody only, and cells stained with an isotype matched control antibody (1B7).

Briefly, approximately 1×10^5 to 5×10^5 cells were aliquoted per well and one antibody per well was added per transfectant. Cells were centrifuged in a table top centrifuge at $1200 \times g$ for five minutes at $4^\circ C$, rinsed in staining buffer (containing ice-cold CMF-PBS 2% FBS), and centrifuged again.

Primary antibody (100 μl at 10 $\mu g/ml$) or staining buffer, was added to each well and incubation carried out on ice for 30 min. Cells were pelleted by centrifugation and washed once with staining buffer. Secondary antibody (100 μl), typically sheep anti-mouse Ig-FITC (Sigma), at a 1:200 dilution was added to each well and incubation carried out on ice in the dark for 30 minutes. Cells were pelleted by centrifugation, washed three times with CMF-PBS, and resuspended and fixed in 300 μl 1% formaldehyde. Samples were analyzed on the same day stained.

Results indicated that the mutants could be separated into four phenotypes: 1) mutants that demonstrated wild type levels of binding with or without 240Q induction (Val¹⁵⁷→Ala, Glu²¹⁸→Ala, Thr²³¹→Ala, Lys²⁸⁰→Ala, and Lys²⁹⁴→Ala), 2) mutants that supported greater than wild type levels of binding without 240Q induction and wild type levels with induction (Ile²³⁵→Ala, Ile²⁵⁵→Ala, Ser²⁸³→Ala, Glu²⁸⁴→Ala, Glu³⁰¹→Ala, and Ile³⁰⁶→Ala), 3) mutants that possessed decreased levels of binding relative to wild type binding in the absence of induction, but wild-type levels with 240Q induction (Lys¹⁶⁰→Ala, Lys²³²→Ala, Asp²⁵³→Ala, Lys²⁸⁷→Ala, Gln³⁰³→Ala, Lys³⁰⁴→Ala, and Lys³⁰⁵→Ala), and 4) mutants that demonstrate severely decreased levels or no binding with or without 240Q (Tyr³⁰⁷→Ala).

The effects of mutations on ICAM-1 binding were not due to varying levels of LFA-1 expression, and both CD11a and CD18 were expressed at equivalent levels to that of wild type. For mutants showing significantly decreased binding, ¹⁵N labeled I domain was prepared and ¹H-¹⁵N HSQC spectra were compared to that of wild type I domain. All of these mutant protein spectra were very similar to that of the wild type protein indicating that no significant conformational changes in the protein arose from any of the mutations. Data for the eighth mutant, K304A, could

not be obtained due to poor expression of the protein in bacteria. These mutants all bound 240Q at equal levels.

The analysis indicates that amino acids in and around the site of antagonist binding contribute to a regulatory site for LFA-1 mediated cell adhesion.

5 The residues Lys²³², Lys²⁸⁷, Lys³⁰⁴, Lys³⁰⁵, and Tyr³⁰⁷ are all hydrophilic residues that surround, but do not directly form, the small molecule ligand binding site. Residues Val¹⁵⁷, Ile²³⁵, Ile²⁵⁵, and Ile³⁰⁶ form the hydrophobic pocket of the small molecule binding site.

10 **6. Mechanism of Regulation**

LFA-1 binding activity is regulated through two different mechanisms which are not mutually exclusive: 1) control of individual receptor affinity (the strength of binding between two molecules), and 2) control of overall avidity (the affinity multiplied by the number of interactions which are occurring at one time) by the regulated aggregation of individual receptors through interactions with the cellular cytoskeleton. If the LFA-1 regulatory binding site, as defined above, is responsible for regulating individual receptor affinity, then the activating mutants, typified by I235A (described above), should possess higher binding affinity in cellular adhesion. These methods, however, are imprecise and do not accurately separate affinity from avidity. Therefore, in order to accurately measure the relative binding affinity of wildtype and mutant I235A for ICAM-1, the following assay was carried out.

Recombinant I235A was produced in CHO cells in secreted form using the same method as that used for production of recombinant LFA-1 in Example 1. The soluble forms of recombinant LFA-1 (used here and in Example 1) and I235A (used here) contain deletions of the transmembrane and cytoplasmic domains of CD11a and CD18 (SEQ ID NO: 30 [full length polynucleotide] and 31 [full length amino acid]), and substitution of these regions for acidic and basic leucine zipper cassettes, respectively, which promote and stabilize specific heterodimerization as described for the production of soluble T-cell receptor [*Hsiu-Ching et al Proc. Natl. Acad. Sci. (USA) 91: 11408-11412 (1994)*].

Both wildtype and mutant I235A CD11a were truncated after position Q1063 in the mature polypeptide, and the 47 amino acid acidic leucine zipper cassette (SEQ ID NO: 32) was added in-frame, using standard methods. CD18 was truncated after position N678 in the mature polypeptide, and the 47 amino acid basic leucine zipper cassette (SEQ ID NO: 33) was added in-frame.

5 Acidic leucine zipper cassette SEQ ID NO: 32

Thr Arg Ser Ser Ala Asp Leu Val Pro Arg Gly Ser Thr Thr Ala Pro Ser Ala Gln Leu
Glu Lys Glu Leu Gln Ala Leu Glu Lys Glu Asn Ala Gln Leu Glu Trp Glu Leu Gln
10 Ala Leu Glu Lys Glu Leu Ala Gln

Basic leucine zipper cassette SEQ ID NO: 33

15 Thr Arg Ser Ser Ala Asp Leu Val Pro Arg Gly Ser Thr Thr Ala Pro Ser Ala Gln Leu
Lys Lys Leu Gln Ala Leu Lys Lys Lys Asn Ala Gln Leu Lys Trp Lys Leu Gln Ala
Leu Lys Lys Leu Ala Gln

Both recombinant LFA-1 and I235A were expressed in CHO cells and purified from the supernatants using separate 8 ml immunoaffinity columns created by coupling 2 mg of anti-CD18 23I11B monoclonal antibody per ml of activated CNBr-Sepharose™

20 according to the manufacturer's suggested protocol, and eluted using a 20 mM Tris (pH 7.5), 2.5 M MgCl₂ buffer. Recombinant LFA-1 and I235A were then purified a second time by gel filtration chromatography over a Pharmacia HiLD SuperDex 200™ column in PBS buffer using standard methods, in order to remove any single chain, aggregated and/or degraded material. The resulting suspensions of purified 25 heterodimers were concentrated using Millipore Ultrafree-4 Centrifugal Filter Units™ with Biomax-30™ membranes, then dialyzed in HBS buffer (10 mM HEPES, pH 7.4, 150 mM NaCl, and 2 mM MgCl₂) at 4 °C, and quantitated using a BioRad Protein Assay™ and the manufacturer's protocol.

The affinity of recombinant LFA-1 and I235A was then measured by 30 surface plasmon resonance using a BIACore 2000 biosensor™ (Pharmacia Biosensor AB). All experiments were performed at 25 °C. All proteins for injection were diluted in HBS buffer. Anti-human Fc antibody (Pierce) was coupled to a CM5™ sensor chip (Pharmacia Biosensor AB) using an amine-coupling kit (Pharmacia

Biosensor AB). The antibody was injected at 50 mg/ml in 10 mM Na acetate (pH 4.5) buffer until approximately 12,000 RU was bound. For each assay, recombinant ICAM-1/IgG1 (see above) was injected at 10 mg/ml until 200 RU was captured onto the chip through binding to the anti-human Fc antibody. LFA-1 or I235A was then injected at different concentrations, using a flow rate of 10 ml/min, and the surface plasmon resonance was recorded. After each concentration of LFA-1 or I235A was allowed to bind and dissociate, the chip was stripped of ICAM-1/LFA-1 complexes with 0.1N HCl and regenerated with fresh ICAM-1/IgG1 before the next concentration of LFA-1 or I235A was analyzed. The association and dissociation rate constants (k_a and k_d , respectively) for LFA-1 and I235A were calculated using the BIA evaluation 2.0 program and its 1:1 Langmuir binding kinetics model (Pharmacia Biosensor AB). The k_a for LFA-1 and I235A were identical and equaled $2.2 \times 10^5 \text{ M}^{-1} \text{ s}^{-1}$. However, the k_d for LFA-1 and I235A were significantly different and equaled $1.2 \times 10^{-2} \text{ s}^{-1}$ and $1.9 \times 10^{-3} \text{ s}^{-1}$, respectively. These values corresponded to an affinity dissociation rate (K_D) of 547 nM for LFA-1, which is in close agreement with the value of 500 nM calculated by Tominaga using a similar method [Tominaga, *et al J. Immunol.*, 161: 4016-4022 (1998)]. However, the corresponding K_D of 86 nM for I235A, represents a 6-fold increase in affinity for I235A over LFA-1, which was similar to the increase observed in cell-binding assays using COS-7 cell transfectants (discussed above). These data strongly suggest that the activation of LFA-1 binding to ICAM-1 caused by the I235A mutation in the LFA-1 regulatory binding site was a result of an increase in LFA-1 affinity. Therefore, the molecular mechanism whereby the LFA-1 regulatory binding site mediates its effects on LFA-1 binding to ICAM, must be effected in large part through regulation of the affinity state of LFA-1. Based on these data, the diaryl sulfide compounds which bind to the LFA-1 regulatory binding site are predicted to inhibit adhesion to ICAM-1 by lowering the affinity of LFA-1 for ICAM through an increase in the k_d of the receptor or through stabilizing the low affinity state of LFA-1.

While the present invention has been described in terms of specific embodiments, it is understood that variations and modifications will occur to those

skilled in the art. Accordingly, only such limitations as appear in the appended claims should be placed on the invention.

WHAT IS CLAIMED IS:

1. A method for identifying a negative regulator of LFA-1 binding to a natural ligand that binds LFA-1 comprising the steps of (i) measuring LFA-1 and ligand binding in the presence and absence of a test compound under conditions that allow binding of LFA-1 to the ligand, (ii) identifying as a negative regulator the test compound which decreases LFA-1 binding to the ligand and which binds LFA-1 α_L polypeptide at a site presenting a conformation that binds a diaryl sulfide or a site defined by Ile²⁵⁹, Leu²⁹⁸, Ile²³⁵, Val¹⁵⁷, Leu¹⁶¹, and Ile³⁰⁶ of human LFA-1.
2. A method for identifying a negative regulator of LFA-1 binding to a natural ligand that binds LFA-1 comprising the steps of (i) measuring LFA-1 and ligand binding in the presence and absence of a test compound under conditions that allow binding of LFA-1 to the ligand, (ii) identifying as a negative regulator the test compound which decreases LFA-1 binding to the ligand and which binds LFA-1 α_L polypeptide at a site that binds a diaryl sulfide or a site defined by Ile²⁵⁹, Leu²⁹⁸, Ile²³⁵, Val¹⁵⁷, Leu¹⁶¹, Ile³⁰⁶, Leu³⁰², Tyr²⁵⁷, Leu¹³², Val²³³, Val¹³⁰, and Tyr¹⁶⁶ of human LFA-1.
3. A method for identifying a negative regulator of LFA-1 binding to a natural ligand that binds LFA-1 comprising the steps of (i) measuring LFA-1 and ligand binding in the presence and absence of a test compound under conditions that allow binding of LFA-1 to the ligand, (ii) identifying as a negative regulator the test compound which decreases LFA-1 binding to the ligand and which binds LFA-1 α_L polypeptide at a site that binds a diaryl sulfide or a site defined by Ile²⁵⁹, Leu²⁹⁸, Ile²³⁵, Val¹⁵⁷, Leu¹⁶¹, Ile³⁰⁶, Lys²⁸⁷, Leu³⁰², Ile²⁵⁷, Lys³⁰⁵, Leu¹⁶¹, Leu¹³², Val²³³, Ile²⁵⁵, Val¹³⁰, Tyr¹⁶⁶, Phe¹³⁴, Phe¹⁶⁸, Phe¹⁵³, Tyr³⁰⁷, Val³⁰⁸, Ile³⁰⁹, Thr²³¹, Glu²⁸⁴, Phe²⁸⁵, Glu³⁰¹, Met¹⁵⁴, Ile²³⁷, Ile¹⁵⁰, and Leu²⁹⁵ of human LFA-1.

4. A method for identifying a negative regulator of LFA-1 binding to a natural ligand that binds LFA-1 comprising the steps of (i) measuring LFA-1 and ligand binding under conditions that allow binding of LFA-1 to the ligand in the presence and absence of a test compound, (ii) identifying as a negative regulator the test compound which decreases LFA-1 binding to the ligand and which competes with (2-isopropyl-phenyl)[2-nitro-4-(E-((4-acetylpiperazin-1-yl)carbonyl)ethenyl)phenyl]sulfide for binding to LFA-1 α_1 polypeptide.

5. A screening method for identifying a negative regulator of LFA-1 binding to a natural ligand that binds LFA-1 comprising the steps of (i) contacting LFA-1 with (2-isopropyl-phenyl)[2-nitro-4-(E-((4-acetylpiperazin-1-yl)carbonyl)ethenyl)phenyl]sulfide in the presence and absence of a compound, and (ii) identifying the compound as a putative negative regulator wherein the compound competes with compound (2-isopropyl-phenyl)[2-nitro-4-(E-((4-acetylpiperazin-1-yl)carbonyl)ethenyl)phenyl]sulfide for binding to LFA-1 α_1 polypeptide.

6. The method according to any one of claim 1 through 5 wherein the natural ligand is an ICAM.

7. The method according to claim 6 wherein the ICAM is ICAM-1 or ICAM-3.

8. The method of claim 1, 2, 3, 4, 5 or 7 wherein the negative regulator is a diaryl sulfide.

9. A pharmaceutical composition comprising a negative regulator of LFA-1 binding to a natural ligand that binds LFA-1 identified by the method of claim 1, 2, 3, 4, or 5.

10. Use of a negative regulator identified by the method of claim 8 in the production of a medicament to ameliorate pathologies arising from LFA-1 binding to a natural ligand that binds LFA-1.

11. A method for inhibiting LFA-1 binding to a natural ligand that binds LFA-1 comprising the step of contacting LFA-1 with a negative regulator compound; said negative regulator binding LFA-1 α_L polypeptide at a site selected from the group consisting of a diaryl sulfide binding conformation defined by Ile²⁵⁹, Leu²⁹⁸, Ile²³⁵, Val¹⁵⁷, Leu¹⁶¹, and Ile³⁰⁶ of human LFA-1 α_L polypeptide and an LFA-1 domain that binds compound (2-isopropyl-phenyl)[2-nitro-4-(E-((4-acetylpirazin-1-yl)carbonyl)ethenyl)phenyl]sulfide .

12. A method to inhibit leukocyte adhesion to endothelial cells comprising the step of contacting said leukocyte with a negative regulator of LFA-1 binding to an ICAM that binds LFA-1, said negative regulator binding an LFA-1 regulatory site selected from the group consisting of a diaryl sulfide binding conformation defined by Ile²⁵⁹, Leu²⁹⁸, Ile²³⁵, Val¹⁵⁷, Leu¹⁶¹, and Ile³⁰⁶ of human LFA-1 α_L polypeptide and an LFA-1 domain that binds compound (2-isopropyl-phenyl)[2-nitro-4-(E-((4-acetylpirazin-1-yl)carbonyl)ethenyl)phenyl]sulfide.

13. A method to ameliorate a pathology arising from LFA-1 binding to a natural ligand that binds LFA-1 comprising the step of administering to an individual in need thereof a negative regulator of LFA-1 binding to the ligand in an amount effective to inhibit LFA-1 binding to the ligand, said negative regulator binding to an LFA-1 regulatory site selected from the group consisting of a diaryl sulfide binding conformation defined by Ile²⁵⁹, Leu²⁹⁸, Ile²³⁵, Val¹⁵⁷, Leu¹⁶¹, and Ile³⁰⁶ of human LFA-1 and an LFA-1 domain that binds compound (2-isopropyl-phenyl)[2-nitro-4-(E-((4-acetylpirazin-1-yl)carbonyl)ethenyl)phenyl]sulfide.

14. The method of claim 9, 10, 11, 12, or 13 wherein the inhibitor is a diaryl sulfide.

15. The method of claim 11 or 13 wherein the natural ligand is an ICAM.

16. The method of claim 15 wherein the ICAM is ICAM-1 or ICAM-3.

17. A mutant LFA-1 α_1 polypeptide comprising an amino acid substitution selected from the group consisting of Val¹⁵⁷-Ala, Glu²¹⁸-Ala, Thr²³¹-Ala, Lys²⁸⁰-Ala, Lys²⁹⁴-Ala, Ile²³⁵-Ala, Ile²⁵⁵-Ala, Ser²⁸³-Ala, Glu²⁸⁴-Ala, Glu³⁰¹-Ala, Ile³⁰⁶-Ala, Lys¹⁶⁰-Ala, Lys²³²-Ala, Asp²⁵³-Ala, Lys²⁸⁷-Ala, Gln³⁰³-Ala, Lys³⁰⁴-Ala, Lys³⁰⁵-Ala, and Tyr³⁰⁷-Ala of SEQ ID NO: 2.

18. A monoclonal antibody secreted by hybridoma 240Q.

SEQUENCE LISTING

<110> Staunton, Donald
Huth, Jeff

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Gly His Cys Leu Pro Val Thr Leu Arg Gly Ser Asn Tyr Thr Ser Lys
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Gly Ser Ile Leu Ala Cys Asp Pro Gly Leu Ser Arg Thr Cys Asp Gln
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225 230 235 240
Glu Ala Thr Asp Ser Gly Asn Ile Asp Ala Ala Lys Asp Ile Ile Arg
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Tyr Ile Ile Gly Ile Gly Lys His Phe Gln Thr Lys Glu Ser Gln Glu
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Thr Leu His Lys Phe Ala Ser Lys Pro Ala Ser Glu Phe Val Lys Ile
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Ser Phe Thr Pro Lys Gly Pro Lys Ile His Gln Val Lys His Met Tyr
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Gln Val Arg Ile Gln Pro Ser Ile His Asp His Asn Ile Pro Thr Leu
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 7
gaaggatgtg atgaaggcgat tcagcaacac ttgc 34

<210> 8
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 8
caattatgtc gcgacacgcgg tgttccggga ggag 34

<210> 9
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 9
gccccggccag atgccgcgaa agtgcttatac atc 33

<210> 10

<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 10
cggccagatg ccaccgcggt gcttatcatc atc

33

<210> 11
<211> 33
<212> DNA
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<220>
<223> Description of Artificial Sequence: primer

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gccacccaaag tgcttgcgt catcacggat ggg

33

<210> 12
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 12
catcgctgcg gccaaagcga tcatccgcta catc

34

<210> 13
<211> 33
<212> DNA
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<220>
<223> Description of Artificial Sequence: primer

<400> 13
gcccccaaaag acatcgcgcg ctacatcatc ggg

33

<210> 14
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 14
cacaatttg catcagcgcc cgcgagcgag tttg

34

<210> 15
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<220>

<223> Description of Artificial Sequence: primer

<400> 15

gcatcaaaac ccgcggcgga gtttgtaaa attc

34

<210> 16

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 16

caaaacccgc gagcgcgtt gtgaaaattc tg

32

<210> 17

<211> 34

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

<400> 17

gcgagcagt ttgtggcgat tctggacaca tttg

34

<210> 18

<211> 33

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

<400> 18

ctggacacat ttgaggcgct gaaagatcta ttc

33

<210> 19

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 19

gaaagatcta ttcaactgaga tgcagaagaa gatc

34

<210> 20

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 20

ctattcacgt gagctggcga agaagatcta tgtc

34

<210> 21

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 21

ttcaactgagc tgcaggcgaa gatctatgtc attg

34

<210> 22

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 22

cactgagctg cagaaggcgaa tctatgtcat tgag

34

<210> 23

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 23

gagctgcaga agaaggcgta tgtcatttag ggc

33

<210> 24

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 24

ctgcagaaga agatcgccgt cattgagggc aca

33

<210> 25

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 25
acggatgggg aggccgcgga cagtggcaac atc

33

<210> 26
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 26
ggggaggcca ctgacgcggg aaacatcgat gc

32

<210> 27
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 27
gccactgaca gtggcgcat cgatgcggcc aaag

34

<210> 28
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 28
gacagtggca acatcgccgc ggccaaagac atc

33

<210> 29
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 29
caacatcgat gccccgcgg acatcatccg ctac

34

<210> 30
<211> 2704
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<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(2307)

<400> 30

atg ctg ggc ctg cgc ccc cca ctg ctc gcc ctg gtg ggg ctg ctc tcc Met Leu Gly Leu Arg Pro Pro Leu Leu Ala Leu Val Gly Leu Leu Ser 1 5 10 15	48
ctc ggg tgc gtc ctc tct cag gag tgc acg aag ttc aag gtc agc agc Leu Gly Cys Val Leu Ser Gln Glu Cys Thr Lys Phe Lys Val Ser Ser 20 25 30	96
tgc cgg gaa tgc atc gag tcg ggg ccc ggc tgc acc tgg tgc cag aag Cys Arg Glu Cys Ile Glu Ser Gly Pro Gly Cys Thr Trp Cys Gln Lys 35 40 45	144
ctg aac ttc aca ggg ccg ggg gat cct gac tcc att cgc tgc gac acc Leu Asn Phe Thr Gly Pro Gly Asp Pro Asp Ser Ile Arg Cys Asp Thr 50 55 60	192
cgg cca cag ctg ctc atg agg ggc tgt gcg gct gac gac atc atg gac Arg Pro Gln Leu Leu Met Arg Gly Cys Ala Ala Asp Asp Ile Met Asp 65 70 75 80	240
ccc aca agc ctc gct gaa acc cag gaa gac cac aat ggg ggc cag aag Pro Thr Ser Leu Ala Glu Thr Gln Glu Asp His Asn Gly Gly Gln Lys 85 90 95	288
cag ctg tcc cca caa aaa gtg acg ctt tac ctg cga cca ggc cag gca Gln Leu Ser Pro Gln Lys Val Thr Leu Tyr Leu Arg Pro Gly Gln Ala 100 105 110	336
gca gcg ttc aac gtg acc ttc cgg cgg gcc aag ggc tac ccc atc gac Ala Ala Phe Asn Val Thr Phe Arg Arg Ala Lys Gly Tyr Pro Ile Asp 115 120 125	384
ctg tac tat ctg atg gac ctc tcc tac tcc atg ctt gat gac ctc agg Leu Tyr Tyr Leu Met Asp Leu Ser Tyr Ser Met Leu Asp Asp Leu Arg 130 135 140	432
aat gtc aag aag cta ggt ggc gac ctg ctc cgg gcc ctc aac gag atc Asn Val Lys Lys Leu Gly Gly Asp Leu Leu Arg Ala Leu Asn Glu Ile 145 150 155 160	480
acc gag tcc ggc cgc att ggc ttc ggg tcc ttc gtg gac aag acc gtg Thr Glu Ser Gly Arg Ile Gly Phe Gly Ser Phe Val Asp Lys Thr Val 165 170 175	528
ctg ccg ttc gtg aac acg cac cct gat aag ctg cga aac cca tgc ccc Leu Pro Phe Val Asn Thr His Pro Asp Lys Leu Arg Asn Pro Cys Pro 180 185 190	576
aac aag gag aaa gag tgc cag ccc ccg ttt gcc ttc agg cac gag ctg Asn Lys Glu Lys Glu Cys Gln Pro Pro Phe Ala Phe Arg His Val Leu 195 200 205	624
aag ctg acc aac aac tcc aac cag ttt cag acc gag gtc ggg aag cag Lys Leu Thr Asn Asn Ser Asn Gln Phe Gln Thr Glu Val Gly Lys Gln 210 215 220	672
ctg att tcc gga aac ctg gat gca ccc gag ggt ggg ctg gac gcc atg Leu Ile Ser Gly Asn Leu Asp Ala Pro Glu Gly Gly Leu Asp Ala Met 225 230 235 240	720
atg cag gtc gcc gcc tgc ccg gag gaa atc ggc tgg cgc aac gtc acg Met Gln Val Ala Ala Cys Pro Glu Glu Ile Gly Trp Arg Asn Val Thr	768

245	250	255	
cg g ct g ct g gt g ttt g c act gat gac g g c t cat ttc g c g g c a c Arg Leu Leu Val Phe Ala Thr Asp Asp Gly Phe His Phe Ala Gly Asp	260	265	816
		270	
g g a a g a ct g g g c g c c atc ct g acc c cc a a c g a c g g c c t g t c a c ct g Gly Lys Leu Gly Ala Ile Leu Thr Pro Asn Asp Gly Arg Cys His Leu	275	280	864
		285	
g a g a c a a c tt g tac a a g agg agc a a c gaa ttc g a c tac c ca t c g gt g Glu Asp Asn Leu Tyr Lys Arg Ser Asn Glu Phe Asp Tyr Pro Ser Val	290	295	912
		300	
g g c c a g ct g g c c a c a a g ct g g c t gaa a a c a a c atc c a g c cc atc t tc Gly Gln Leu Ala His Lys Leu Ala Glu Asn Asn Ile Gln Pro Ile Phe	305	310	960
		315	
g c g gt g acc agt agg at g gt g a a g acc tac gag aaa c tc acc gag atc Ala Val Thr Ser Arg Met Val Lys Thr Tyr Glu Lys Leu Thr Glu Ile	325	330	1008
		335	
atc c cc c a a g t c a g cc g t g g gg g a g ct g t c t g a c t c c a a t g t g Ile Pro Lys Ser Ala Val Gly Glu Leu Ser Glu Asp Ser Ser Asn Val	340	345	1056
		350	
gt c .cat c tc att a a g a a t g c t tac a a t aaa c tc t c c t c c agg g t c t tc Val His Leu Ile Lys Asn Ala Tyr Asn Lys Leu Ser Ser Arg Val Phe	355	360	1104
		365	
ct g gat cac a a c g cc c tc c cc g a c acc ct g aaa g t c acc tac g a c t c c Leu Asp His Asn Ala Leu Pro Asp Thr Leu Lys Val Thr Tyr Asp Ser	370	375	1152
		380	
t tc t gc agc a a t g g a g t g ac g c a c agg a a c c a g c cc a g a g g t g a c t gt Phe Cys Ser Asn Gly Val Thr His Arg Asn Gln Pro Arg Gly Asp Cys	385	390	1200
		395	
g a t g g c g t g c a g atc a a t g t c c cg atc acc t tc c a g g t g a a g g t c ac g Asp Gly Val Gln Ile Asn Val Pro Ile Thr Phe Gln Val Lys Val Thr	405	410	1248
		415	
g cc a ca g a g t gc atc c a g g a g c a g t cg t tt g tc atc c gg g cc ct g g gc Ala Thr Glu Cys Ile Gln Glu Gln Ser Phe Val Ile Arg Ala Leu Gly	420	425	1296
		430	
t tc ac g g a c at a g t g acc g t g c a g g t t c tt c cc c a g t gt g a g t gc c gg Phe Thr Asp Ile Val Thr Val Gln Val Leu Pro Gln Cys Glu Cys Arg	435	440	1344
		445	
t gc c gg g a c c a g a g a g a c c gc a g c c tc t gc cat g gc a a g g g c t tc Cys Arg Asp Gln Ser Arg Asp Arg Ser Leu Cys His Gly Lys Gly Phe	450	455	1392
		460	
tt g g a g t gc g g c atc t gc agg t gt g a c act g g c tac att g gg aaa a a c Leu Glu Cys Gly Ile Cys Arg Cys Asp Thr Gly Tyr Ile Gly Lys Asn	465	470	1440
		475	
t gt g a g t gc c a g a c a c g g g g c c gg a g c a g c c ag g g a g g a a g c Cys Glu Cys Gln Thr Gln Gly Arg Ser Ser Gln Glu Leu Glu Gly Ser	485	490	1488
		495	

tgc	cg	aag	gac	aac	tcc	atc	atc	tgc	tca	ggg	ctg	ggg	gac	tgt	1536	
Cys	Arg	Lys	Asp	Asn	Asn	Ser	Ile	Ile	Cys	Ser	Gly	Leu	Gly	Asp	Cys	
500															510	
gtc	tgc	ggg	cag	tgc	ctg	tgc	cac	acc	agc	gac	gtc	ccc	ggc	aag	ctg	1584
Val	Cys	Gly	Gln	Cys	Leu	Cys	His	Thr	Ser	Asp	Val	Pro	Gly	Lys	Leu	
515															525	
ata	tac	ggg	cag	tac	tgc	gag	tgt	gac	acc	atc	aac	tgt	gag	cgc	tac	1632
Ile	Tyr	Gly	Gln	Tyr	Cys	Glu	Cys	Asp	Thr	Ile	Asn	Cys	Glu	Arg	Tyr	
530															540	
aac	ggc	cag	gtc	tgc	ggc	ggc	ccg	ggg	agg	ggg	ctc	tgc	ttc	tgc	ggg	1680
Asn	Gly	Gln	Val	Cys	Gly	Gly	Pro	Gly	Arg	Gly	Leu	Cys	Phe	Cys	Gly	
545															560	
aag	tgc	cgc	tgc	cac	ccg	ggc	ttt	gag	ggc	tca	gcg	tgc	cag	tgc	gag	1728
Lys	Cys	Arg	Cys	His	Pro	Gly	Phe	Glu	Gly	Ser	Ala	Cys	Gln	Cys	Glu	
565															575	
agg	acc	act	gag	ggc	tgc	ctg	aac	ccg	cg	gt	gag	tgt	agt	ggt	1776	
Arg	Thr	Thr	Glu	Gly	Cys	Leu	Asn	Pro	Arg	Arg	Val	Glu	Cys	Ser	Gly	
580															590	
cgt	ggc	cgg	tgc	cgc	tgc	aac	gta	tgc	gag	tgc	cat	tca	ggc	tac	cag	1824
Arg	Gly	Arg	Cys	Arg	Cys	Asn	Val	Cys	Glu	Cys	His	Ser	Gly	Tyr	Gln	
595															605	
ctg	cct	ctg	tgc	cag	gag	tgc	ccc	ggc	tgc	ccc	tca	ccc	tgt	ggc	aag	1872
Leu	Pro	Leu	Cys	Gln	Glu	Cys	Pro	Gly	Cys	Pro	Ser	Pro	Cys	Gly	Lys	
610															620	
tac	atc	tcc	tgc	gcc	gag	tgc	ctg	aag	ttc	gaa	aag	ggc	ccc	ttt	ggg	1920
Tyr	Ile	Ser	Cys	Ala	Glu	Cys	Leu	Lys	Phe	Glu	Lys	Gly	Pro	Phe	Gly	
625															640	
aag	aac	tgc	agc	gcf	gcf	tgt	ccg	ggc	ctg	cag	ctg	tcg	aac	aac	ccc	1968
Lys	Asn	Cys	Ser	Ala	Ala	Cys	Pro	Gly	Leu	Gln	Leu	Ser	Asn	Asn	Pro	
645															655	
gtg	aag	ggc	agg	acc	tgc	aag	gag	agg	gac	tca	gag	ggc	tgc	tgg	gtg	2016
Val	Lys	Gly	Arg	Thr	Cys	Lys	Glu	Arg	Asp	Ser	Glu	Gly	Cys	Trp	Val	
660															670	
gcc	tac	acg	ctg	gag	cag	cag	gac	ggg	atg	gac	cgc	tac	ctc	atc	tat	2064
Ala	Tyr	Thr	Leu	Glu	Gln	Gln	Asp	Gly	Met	Asp	Arg	Tyr	Leu	Ile	Tyr	
675															685	
gtg	gat	gag	agc	cga	gag	tgt	gtg	gca	ggc	ccc	aac	atc	gcc	gcc	atc	2112
Val	Asp	Glu	Ser	Arg	Glu	Cys	Val	Ala	Gly	Pro	Asn	Ile	Ala	Ala	Ile	
690															700	
tgc	ggg	ggc	acc	gtg	gca	ggc	atc	gtg	ctg	atc	ggc	att	ctc	ctg	ctg	2160
Val	Gly	Gly	Thr	Val	Ala	Gly	Ile	Val	Leu	Ile	Gly	Ile	Leu	Leu	Leu	
705															720	
tgc	atc	tgg	aag	gct	ctg	atc	cac	ctg	agc	gac	ctc	cg	gag	tac	agg	2208
Val	Ile	Trp	Lys	Ala	Leu	Ile	His	Leu	Ser	Asp	Leu	Arg	Glu	Tyr	Arg	
725															735	
cgc	ttt	gag	aag	gag	aag	ctc	aag	tcc	cag	tgg	aac	aat	gat	aat	ccc	2256
Arg	Phe	Glu	Lys	Glu	Lys	Ser	Gln	Trp	Asn	Asn	Asp	Asn	Pro			

740

745

750

ctt ttc aag agc gcc acc acg acg gtc atg aac ccc aag ttt gct gag	2304
Leu Phe Lys Ser Ala Thr Thr Thr Val Met Asn Pro Lys Phe Ala Glu	
755	760
765	
agt taggagcaact tggtaagac aaggccgtca ggaccacca tgtctcccc	2357
Ser	
atcacgcggc cgagacatgg cttggccaca gctctgagg atgtcaccaa ttaaccagaa	2417
atccagttat ttccgcctt caaatgaca gccatggccg gccggtgctt ctgggggctc	2477
gtcgaaaaa cagctccact ctgactggca cagtcttgc atggagactt gaggaggct	2537
ttaggtaggt gaggttaggt gcgtgttcc tgtgcaagtc aggacatcag tctgattaaa	2597
ggtgtgtcca atttatttac atttaaactt gtcagggtat aaaatgacat cccattaatt	2657
atattgttaa tcaatcacgt gtatagaaaa aaaaataaaaa cttcaat	2704

<210> 31
<211> 769
<212> PRT
<213> Homo sapiens

<400> 31			
Met Leu Gly Leu Arg Pro Pro Leu Leu Ala Leu Val Gly Leu Leu Ser			
1	5	10	15
Leu Gly Cys Val Leu Ser Gln Glu Cys Thr Lys Phe Lys Val Ser Ser			
20	25	30	
Cys Arg Glu Cys Ile Glu Ser Gly Pro Gly Cys Thr Trp Cys Gln Lys			
35	40	45	
Leu Asn Phe Thr Gly Pro Gly Asp Pro Asp Ser Ile Arg Cys Asp Thr			
50	55	60	
Arg Pro Gln Leu Leu Met Arg Gly Cys Ala Ala Asp Asp Ile Met Asp			
65	70	75	80
Pro Thr Ser Leu Ala Glu Thr Gln Glu Asp His Asn Gly Gly Gln Lys			
85	90	95	
Gln Leu Ser Pro Gln Lys Val Thr Leu Tyr Leu Arg Pro Gly Gln Ala			
100	105	110	
Ala Ala Phe Asn Val Thr Phe Arg Arg Ala Lys Gly Tyr Pro Ile Asp			
115	120	125	
Leu Tyr Tyr Leu Met Asp Leu Ser Tyr Ser Met Leu Asp Asp Leu Arg			
130	135	140	
Asn Val Lys Lys Leu Gly Gly Asp Leu Leu Arg Ala Leu Asn Glu Ile			
145	150	155	160
Thr Glu Ser Gly Arg Ile Gly Phe Gly Ser Phe Val Asp Lys Thr Val			
165	170	175	
Leu Pro Phe Val Asn Thr His Pro Asp Lys Leu Arg Asn Pro Cys Pro			

180	185	190
Asn Lys Glu Lys Glu Cys Gln Pro	Pro Phe Ala Phe Arg His Val Leu	
195	200	205
Lys Leu Thr Asn Asn Ser Asn Gln Phe Gln Thr Glu Val Gly Lys Gln		
210	215	220
Leu Ile Ser Gly Asn Leu Asp Ala Pro Glu Gly Gly Leu Asp Ala Met		
225	230	235
Met Gln Val Ala Ala Cys Pro Glu Glu Ile Gly Trp Arg Asn Val Thr		
245	250	255
Arg Leu Leu Val Phe Ala Thr Asp Asp Gly Phe His Phe Ala Gly Asp		
260	265	270
Gly Lys Leu Gly Ala Ile Leu Thr Pro Asn Asp Gly Arg Cys His Leu		
275	280	285
Glu Asp Asn Leu Tyr Lys Arg Ser Asn Glu Phe Asp Tyr Pro Ser Val		
290	295	300
Gly Gln Leu Ala His Lys Leu Ala Glu Asn Asn Ile Gln Pro Ile Phe		
305	310	315
Ala Val Thr Ser Arg Met Val Lys Thr Tyr Glu Lys Leu Thr Glu Ile		
325	330	335
Ile Pro Lys Ser Ala Val Gly Glu Leu Ser Glu Asp Ser Ser Asn Val		
340	345	350
Val His Leu Ile Lys Asn Ala Tyr Asn Lys Leu Ser Ser Arg Val Phe		
355	360	365
Leu Asp His Asn Ala Leu Pro Asp Thr Leu Lys Val Thr Tyr Asp Ser		
370	375	380
Phe Cys Ser Asn Gly Val Thr His Arg Asn Gln Pro Arg Gly Asp Cys		
385	390	395
Asp Gly Val Gln Ile Asn Val Pro Ile Thr Phe Gln Val Lys Val Thr		
405	410	415
Ala Thr Glu Cys Ile Gln Glu Gln Ser Phe Val Ile Arg Ala Leu Gly		
420	425	430
Phe Thr Asp Ile Val Thr Val Gln Val Leu Pro Gln Cys Glu Cys Arg		
435	440	445
Cys Arg Asp Gln Ser Arg Asp Arg Ser Leu Cys His Gly Lys Gly Phe		
450	455	460
Leu Glu Cys Gly Ile Cys Arg Cys Asp Thr Gly Tyr Ile Gly Lys Asn		
465	470	475
Cys Glu Cys Gln Thr Gln Gly Arg Ser Ser Gln Glu Leu Glu Gly Ser		
485	490	495
Cys Arg Lys Asp Asn Asn Ser Ile Ile Cys Ser Gly Leu Gly Asp Cys		
500	505	510

Val Cys Gly Gln Cys Leu Cys His Thr Ser Asp Val Pro Gly Lys Leu
 515 520 525
 Ile Tyr Gly Gln Tyr Cys Glu Cys Asp Thr Ile Asn Cys Glu Arg Tyr
 530 535 540
 Asn Gly Gln Val Cys Gly Gly Pro Gly Arg Gly Leu Cys Phe Cys Gly
 545 550 555 560
 Lys Cys Arg Cys His Pro Gly Phe Glu Gly Ser Ala Cys Gln Cys Glu
 565 570 575
 Arg Thr Thr Glu Gly Cys Leu Asn Pro Arg Arg Val Glu Cys Ser Gly
 580 585 590
 Arg Gly Arg Cys Arg Cys Asn Val Cys Glu Cys His Ser Gly Tyr Gln
 595 600 605
 Leu Pro Leu Cys Gln Glu Cys Pro Gly Cys Pro Ser Pro Cys Gly Lys
 610 615 620
 Tyr Ile Ser Cys Ala Glu Cys Leu Lys Phe Glu Lys Gly Pro Phe Gly
 625 630 635 640
 Lys Asn Cys Ser Ala Ala Cys Pro Gly Leu Gln Leu Ser Asn Asn Pro
 645 650 655
 Val Lys Gly Arg Thr Cys Lys Glu Arg Asp Ser Glu Gly Cys Trp Val
 660 665 670
 Ala Tyr Thr Leu Glu Gln Gln Asp Gly Met Asp Arg Tyr Leu Ile Tyr
 675 680 685
 Val Asp Glu Ser Arg Glu Cys Val Ala Gly Pro Asn Ile Ala Ala Ile
 690 695 700
 Val Gly Gly Thr Val Ala Gly Ile Val Leu Ile Gly Ile Leu Leu Leu
 705 710 715 720
 Val Ile Trp Lys Ala Leu Ile His Leu Ser Asp Leu Arg Glu Tyr Arg
 725 730 735
 Arg Phe Glu Lys Glu Lys Leu Lys Ser Gln Trp Asn Asn Asp Asn Pro
 740 745 750
 Leu Phe Lys Ser Ala Thr Thr Val Met Asn Pro Lys Phe Ala Glu
 755 760 765

Ser

<210> 32
 <211> 47
 <212> PRT
 <213> Homo sapiens

<400> 32
 Thr Arg Ser Ser Ala Asp Leu Val Pro Arg Gly Ser Thr Thr Ala Pro
 1 5 10 15

Ser Ala Gln Leu Glu Lys Glu Leu Gln Ala Leu Glu Lys Glu Asn Ala

20

25

30

Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Leu Ala Gln
35 40 45

<210> 33

<211> 47

<212> PRT

<213> Homo sapiens

<400> 33

Thr Arg Ser Ser Ala Asp Leu Val Pro Arg Gly Ser Thr Thr Ala Pro
1 5 10 15

Ser Ala Gln Leu Lys Lys Lys Leu Gln Ala Leu Lys Lys Lys Asn Ala
20 25 30

Gln Leu Lys Trp Lys Leu Gln Ala Leu Lys Lys Lys Leu Ala Gln
35 40 45